

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2003, 22:48:30 ; Search time 5084 Seconds
(without alignments)
13027.084 Million cell updates/sec

Title: US-10-054-678-1
Perfect score: 2725
Sequence: 1 tcagtcgtggccagcctg.....aagtcacacttggctggc 2725

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

Database :

EST:*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estmu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hc.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hc.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_man.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	980.6	36.0	1201	9	AL517921
2	953.2	35.0	1201	13	BX404004
3	927.2	34.0	1192	9	AL515786
4	900.6	33.0	1201	9	AL515787

78	397.8	14.6	638	12	BG965999	BG965999 602829793
79	390	14.3	508	9	AW78401	AW78401 119530 MA
80	378.4	13.9	435	10	BE382659	BE382659 601297313
81	374.6	13.7	491	10	BE262329	BE262329 601152211
82	323.4	11.9	440	10	BE314345	BE314345 601147067
83	310	11.4	694	13	BX416107	BX416107 BX416107
84	304.2	11.2	542	10	BF525224	BF525224 UT-R-AB1-
85	300.6	11.0	311	9	AA349106	AA349106 EST55691
86	271	9.9	423	9	AI386204	AI386204 mg4c06.y
87	271	9.9	434	9	AA142680	AA142680 mg4c06.x
88	262.2	9.6	1289	10	BF316992	BF316992 601903955
89	260.6	9.6	477	14	CA364439	CA364439 639338 NC
90	238.2	8.7	1108	13	BU384712	BU384712 603858882
91	229	8.4	315	12	BI976348	BI976348 485196 MA
92	211.6	7.8	254	14	T27961	T27961 EST1967 Hu
93	207.6	7.6	338	13	BY127879	BY127879 BY127879
94	175.8	6.5	2160	11	AK081586	AK081586 Mus muscu
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97	164.4	6.0	167	10	BF311282	BF311282 601896667
98	164	6.0	179	9	AA329415	AA329415 EST33021
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c 100	151.4	5.6	291	9	AW505180	AW505180 UT-HF-BN0
c 101	143.2	5.3	222	14	T11501	T11501 CHR90067 Ch
c 102	141.2	5.2	624	28	AZ366751	AZ366751 IM0116D11
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109	103	3.8	519	4	BX512116	BX512116 RZPD Mus
110	102	3.7	886	13	BU543008	BU543008 AGENCOURT
111	101.2	3.7	915	13	BX390150	BX390150 BX390150
112	98	3.6	801	13	BX315600	BX315600 BX315600
113	90.6	3.3	830	10	BF159611	BF159611 601767217
114	87	3.2	532	12	BI514653	BI514653 BB160015B
115	86.4	3.2	489	12	BI320021	BI320021 ie46h03.y
c 116	84.8	3.1	961	23	CNS03RBC	AL257025 Tetradon
c 117	84.2	3.1	734	13	BX261734	BX261734 BX261734
118	83.8	3.1	520	9	AI892295	AI892295 mm25G09.y
c 119	82.6	3.0	704	14	CD218235	CD218235 pgrin.pk0
120	82.2	3.0	981	10	BF167377	BF167377 601773665

ALIGNMENTS

RESULT 1	AL517921	1201 bp	mRNA	linear	EST 12-MAY-2003
LOCUS	AL517921	1201 bp	mRNA	linear	EST 12-MAY-2003
DEFINITION	AL517921 Homo sapiens NEUROBLASTOMA				
ACCESSION	CS0DA004YB14				
VERSION	AL517921				
KEYWORDS	EST.				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
REFERENCE	1				
AUTHORS	Li W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12781414.				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	BP 191 91006 EVRY cedex - France				
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr				
	Library was constructed by Life Technologies, a division of				
	Invitrogen. This sequence belongs to sequence cluster 5245.f For				
	more information about this cluster, see				
	http://www.genoscope.cns.fr/				

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	/tissue type="NEUROBLASTOMA"	
	/clone_lib="Homo sapiens NEUROBLASTOMA"	
	/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."	
BASE COUNT	225 a 374 c 326 g 215 t	61 others
ORIGIN		
Query Match	36.0%; Score 980.6; DB 9; Length 1201;	
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Matches 1029;	Conservative 44; Mismatches 51; Indels 4; Gaps 4;	
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Qy	66 TGGTGGCCGACATGACAGGCTCGGCTCCCGGTGAGAGCCCTCCCTCATCATCATCCCC 125	
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Qy	185 ATTTCAGCTCTGTGTCGAGAGCTCAAGGCTGGGCTCTGTGTTGGAGTGTCCGACCGTG 244	
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Qy	268 GCGAGCTTCGAGAACGAGATCTCGTGGTCTCTGAGCCGATGGGACATGCTCTATTG 327	
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Qy	305 CGGACCCCTGGAGTGCACCAAGAGGCGAGATCCACCTGGATCCCGACAGGACTACGAGC 364	
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Qy	545 AGAGGGTGCAGCTCTGGAAGCCCAATATCCCGAACCCGAGTTGCCCTCAGAGCGTGA 604	
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Qy	605 CCATGAGGTCCAAGCTCCCAATATCCAGATCCCGAGCAGGAGACCATGTTGTTGCT 664	
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Qy	688 ACATTAAGAGCTTCCAAAGGGCTTCTCTCGGCACCAATATCAAGTACGAGCCCATCG 747	
Db		
Qy	665 ACATTAAGAGCTTCCAAAGGGCTTCTCTCGGCACCAATATCAAGTACGAGCCCATCG 724	
Db		
Qy	748 TCACCAAGGGCAATAGAGCCCTTGTGCACCAATGGAAGTCTTCAGTGGGCCCCGAGA 807	
Db		
Qy	725 TCACCAAGGGCAATAGAGCCCTTGTGCACCAATGGAAGTCTTCAGTGGGCCCCGAGA 784	
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Qy	808 TGGACAGCGTCCCCCACTTTCAGGGGGCTTCGAGTCCCAAGATGAAACCCGAGCCGCTCA 867	
Db		

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Db      785 TGGACAGCGTCCCCCAGCTTCAGCGGGCCCTGGGACTCCMAGATGAACCCGACCGCCTCA 844
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Qy      928 AGGAAGCGCGGCTTCCCTTC-GGGGGTCCAGGGTCTCCAGATATCTCCGCTCGAAGTT 986
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Qy      1107 CCAGTGATGGCACTTCCACACGGGAGACCGCTTTCATCTCCTACTGCTACTGCAACGAC 1166
Db      1084 VCMRTWATGSSCATTTCCACMCGGNGR-CSYTTTCWTCCYCCCTTGTMTGACGGCAA 1142
Qy      1167 AAGTGCAACCACTGGCACTGCCTCCCTCCGGATCCACATCTTCGCC 1214
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RESULT 2
LOCUS   BX404004                      1201 bp      mRNA      linear      EST 13-MAY-2003
DEFINITION   BX404004 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ACCESSION   BX404004
VERSION     BX404004.1 GI:30651929
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
AUTHORS     Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL     Full-length cDNA libraries and normalization
COMMENT     Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB0112C07RP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB0112C07RP1.
FEATURES
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/db_xref="taxon:9606"
/clone="CL0BB0112C07"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      227 a      362 c      331 g      229 t      52 others
ORIGIN
Query Match      35.0%; Score 953.2; DB 13; Length 1201;

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Best Local Similarity 96.1%; Pred. No. 4e-196;
Matches 982; Conservative 14; Mismatches 24; Indels 2; Gaps 2;
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Qy      61 CAGCAGTGGCCATCTTCTGCTCATCTCTGCTGCGGCGCATCTGAGGGCTCGGCTCCCGGTG 120
Db      104 CAGCAGTGGCCATCTTCTGCTCATCTCTGCTGCGGCGCATCTGAGGGCTCGGCTCCCGGTG 163
Qy      121 AGAGCCCTCTCCCTATCATCTCCCTGHAACCGGAGGGTCTCCTGAGACTCTCATGGA 180
Db      164 AGAGCCCTCTCCCTATCATCTCCCTTGGACCGGGA-GGGTCTCTGAGCTCTCATGGA 222
Qy      181 ATGTGAGTACACCCAGGAGGCGCATCTATTTCCAGCTCTCTGCTGGGAGGCTCAAGGCTG 240
Db      223 ATGTGAGTACACCCAGGAGGCGCATCTATTTCCAGCTCTCTGCTGGGAGGCTCAAGGCTG 282
Qy      241 GCGTCTCTTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGAGATCTCTGTTGCTCT 300
Db      283 GCGTCTCTTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGAGATCTCTGTTGCTCT 342
Qy      301 GGACCGATGGGGAACACTGCTCTATTTTGGGAGCGCTGAGTGACAGAGGGGAGATCC 360
Db      343 GGACCGATGGGGAACACTGCTCTATTTTGGGAGCGCTGAGTGACAGAGGGGAGATCC 402
Qy      361 ACCTGGATCCCGAGCAGGACTACCGAGCTGCTGAGGTGCGAGGACCCCAAGGCGCTGA 420
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Qy      1021 AC 1022

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RESULT 6
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DEFINITION AL526121 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
          cDNA clone CS0DC015YD20 5-PRIME, mRNA sequence.
ACCESSION AL526121
VERSION   AL526121.2 GI:31063982
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 993)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12789614.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC015DB10Q1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC015DB10Q1.

FEATURES
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 200 a 316 c 284 g 183 t 10 others
ORIGIN

Query Match 32.3%; Score 879; DB 9; Length 993;
Best Local Similarity 98.3%; Pred. No. 4.6e-180;
Matches 909; Conservative 9; Mismatches 4; Indels 3; Gaps 3;

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Db      311 GGTCTCTGTTGGGATGTCGACCGTGGCGAGCTTCAGAACCGCAGATCTCGTGTGCTCT 370
QY      301 GGACCGATGGGACACTGCTATTTTGGGAGCGCTGGAGTGACCAAGGGGCGAGATCC 360
Db      371 GGACCGATGGGACACTGCTATTTTGGGAGCGCTGGAGTGACCAAGGGGCGAGATCC 430
QY      361 ACCTGATCCCGAGGAGACTACAGCTGTCAGGTGTCAGAGGAGGAGGAGGCTGA 420
Db      431 ACCTGATCCCGAGGAGACTACAGCTGTCAGGTGTCAGAGGAGGAGGAGGCTGA 490
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QY      481 GCACCTGTCACCTTGGTCTACGGGATCCTGGAGAGCGCTTCCGGTCACTGGAGGCCATCA 540
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LOCUS
DEFINITION AL526065 980 bp mRNA linear EST 23-MAY-2003
CDNA clone CS0DC015Y20 3-PRIME, mRNA sequence.
ACCESSION AL526065
VERSION AL526065.2 GI:31063926
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 980)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12789558.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC015DB10NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC015DB10NP1.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC015Y20"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notice="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 187 a 263 c 337 g 153 t 40 others
ORIGIN

Query Match 32.2%; Score 877; DB 9; Length 980;
Best Local Similarity 93.4%; Pred. No. 1.2e-179;
Matches 902; Conservative 26; Mismatches 36; Indels 2; Gaps 2;

Qy 1425 GGGGGCTTCGGGATCTTGGAGGAGATGTGTCAACTACCTGACACTACTACCCCGACAGC 1484
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
979 GTGGGGGTTTCBMTCTCTGGGMCCTKIGTGTGCGCMCGTGTCTTCCCTTCCCGCGMCG 920

Qy 1485 CAGCTGAGCTCTGCAAGACGGCTGTGGACCGCGGCTTCTCGAGAGTACTTCCACCTC 1544
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
919 CAGCTGAGCTCTGCMAGMCGCTGTGSMCGCGGCTTCTCGAGMAGTACTTCCMCTC 860

Qy 1545 ATCAACAGGTTCAACACGAGGATGTGTGACCTGCGCTCAGCGTCCGTGTTCTAGAG 1604
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
859 ATCAACAGGTTCAACACGAGGATGTGTGCMCTGCGCTCAGCGTCCGTGTTCTAGAG 800

Qy 1605 TTCACTCTGTCTCCCTGGAACTCTTCAACCGCGAGTACTGAAGCGCTGTACACCTTC 1664
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
799 TTCACCTCTGTCTCCCTGGMACTCTTCAACCGGAGTACTGAAGCGCTGT-MACMGTC 741

Qy 1665 GCGCCATCTCCATGCACTGCACCAAGTCTTCAGCGTCCGTTCAGGGTGAATGAAC 1724
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
740 GCGCCATCTCCATGCACTGCMAAAGTCTTCAGCGTCCGTTCAGGGTGAATGAAC 681

Qy 1725 CTGACGCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCCACCCACAGTGGCCCCACC 1784
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
680 CTGACGCCCTGCCCAAGGTCATCTCCACACTGGAAGAGCCACCCACAGTGGCCCCACC 621

Qy 1785 AGCCAGGCGCAAGCCCTGCTGCCCCACCGTTGTGACGATTTGGTGGGGGCAAGAGCTGA 1844
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
620 AGCCAGGCGCAAGCCCTGCTGCCCCACCGTTGTGACGATTTGGTGGGGGCAAGAGCTGA 561

FEATURES
source
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Qy 1845 GGGGGGACCTACTCTCTCCCTCTCTCATCTGTCTCCCTGTGGGTACACCGGACCTGTG 1904
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
560 GGGGGGACCTACTCTCTCCCTCTCTCATCTGTCTCCCTGTGGGTACACCGGACCTGTG 501

Qy 1905 CACTTACTCTGGGACGATCCCATGGAAACAGCCCTGTGCACGCCAGGATGAAGGGCCAG 1964
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
500 CACTTACTCTGGGACGATCCCATGGAAACAGCCCTGTGCATGCCAGGATGAAGGGCCAG 441

Qy 1965 ACCACGCCCTGTGCTGAGACCGGTCCTATCCAGCTTCTTCCCGCAGGTTCCCTGCA 2024
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
440 ACCACGCCCTGTGCTGAGACCGGTCCTATCCAGCTTCTTCCCGCAGGTTCCCTGCA 381

Qy 2025 TGCTGAGAGGGTGTGGGTGCTTGTGACCTACCTGGACCGAGTGGACCACTCTCG 2084
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
380 TGCTGAGAGGGTGTGGGTGCTTGTGACCTACCTGGACCGAGTGGACCACTCTCG 321

Qy 2085 TCCATTTAAACCCGGCTGACTCAGTGCAGGACAGCCCGACAGTGGTCCAGGTTCCAGC 2144
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
320 TCCATTTAAACCCGGCTGACTCAGTGCAGGACAGCCCTGCACAGTGGTCCAGGTTCCAGC 261

Qy 2145 CTTCGCCACGACCTGTTCGGCTCTACTGGGTGTGGCTGTGCTTCTGGACAGGACCATG 2204
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
260 CTTCGCCACGACCTGTTCGGCTCTACTGGGTGTGGCTGTGCTTCTGGACAGGACCATG 201

Qy 2205 CTGGCGCGGGGTGTGAATCAACCGGAAACGCCCGCCCGCTGCTTCCCGGTGT 2264
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
200 CTGGCGCGGGGTGTGAATCAACCGGAAACGCCCGCCCGCTGCTTCCCGGTGT 141

Qy 2265 GCAGCGGGTGGGGTGGCGCTTAAACATTTCCCTGCTGAGTGGCTGTGTTTACAGTGG 2324
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140 GCAGCGGGTGGGGTGGCGCTTAAACATTTCCCTGCTGAGTGGCTGTGTTTACAGTGG 82

Qy 2325 GCGGCTTCCCTGCGAGCGGAGGACGAGGACATTTAGTCTAGAGACTCGCTGGGA 2384
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 GCGGCTTCCCTGCGAGCGGAGGACGAGGACGAGGACATTTAGTCTAGAGACTCGCTGGGA 22

Qy 2385 AATTGC 2390
Db |||||
21 TTTTCC 16

RESULT 9
AL524359 948 bp mRNA linear EST 22-MAY-2003
LOCUS AL524359 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DC006YB08 5-PRIME, mRNA sequence.
ACCESSION AL524359
VERSION AL524359.2 GI:31042620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 13, 2001 this sequence version replaced gi:12787852.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC006DA04QPI&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC006DA04QPI.
Location/Qualifiers
1..948

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC06YB08"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      184 a   313 c   263 g   181 t   7 others
ORIGIN

Query Match      32.1%; Score 874.2; DB 9; Length 948;
Best Local Similarity 98.6%; Pred. No. 5e-179;
Matches 873; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1333 GCATGTTCAAGAGGTCTGTGGTCCATCCGGAGATGTCATACCTCTTCGACGT 1392
Db      |||||||
Qy 64   GCATGTTGAAGAGGTCTGTGGTCCATCCGGAGATGTCATACCTCTTCGACGT 123
Db      |||||||
Qy 1393 ACAACACGAAGACCGGAGCTGGCCACAGTGGGGGCTTCGGGATCTGGAGGAGATGT 1452
Db      |||||||
Qy 124   ACACACGAAGACCGGAGCTGGCCACAGTGGGGGCTTCGGATCTCGAGGAGATGT 183
Db      |||||||
Qy 1453 GTGTCAACTAGTGCATCTACTACCCCAAGACGAGCTGGAGCTCTGCAAGACGGCTGTGG 1512
Db      |||||||
Qy 184   GTGTAACTAGTGCATCTACTACCCCAAGACGAGCTGGAGCTCTGCAAGAGCGCTGTGG 243
Db      |||||||
Qy 1513 ACGGCGGCTTCTGCAGAGTACTTCCACCTCATCACAGTTCAACAGGATGTCT 1572
Db      |||||||
Qy 244   ACGGCGGCTTCTGCAGAGTACTTCCACCTCATCACAGTTCAACAGGATGTCT 303
Db      |||||||
Qy 1573 GCACCTGGCTTCAGCGCTCGGTCTCAGCAGTGTCACTCTGTTCCTGGAACCTCTTCA 1632
Db      |||||||
Qy 304   GCACCTGGCTTCAGCGCTCGGTCTCAGCAGTGTCACTCTGTTCCTGGAACCTCTTCA 363
Db      |||||||
Qy 1633 ACCGCGAGTACTGAAGCCCTGTACAGCTTCCGCCCCATCTCCATGCATCTGCAACAAGT 1692
Db      |||||||
Qy 364   ACCGCGAGTACTGAAGCCCTGTACAGCTTCCGCCCCATCTCCATGCATCTGCAACAAGT 423
Db      |||||||
Qy 1693 CTTAGCGCTCGCTTCCAGGGTGAATGGAACTTCGAGCCCTCGCCCAAGTCACTTCCA 1752
Db      |||||||
Qy 424   CTTAGCGCTCGCTTCCAGGGTGAATGGAACTTCGAGCCCTCGCCCAAGTCACTTCCA 483
Db      |||||||
Qy 1753 CACTGGAAGAGCCCAACCCCAAGTGCCCAACAGCCAGGCGCGAAGCCTCTGCGCCCCA 1812
Db      |||||||
Qy 484   CACTGGAAGAGCCCAACCCCAAGTGCCCAACAGCCAGGCGCGAAGCCTCTGCGCCCCA 543
Db      |||||||
Qy 1813 CCCTGTGTCAGCATTTGGTGGGGCAAGGCTGAGGGGGACCTACTCTCTCCCTCTCTCCA 1872
Db      |||||||
Qy 544   CCCTGTGTCAGCATTTGGTGGGGCAAGGCTGAGGGGGACCTACTCTCTCCCTCTCTCCA 603
Db      |||||||
Qy 1873 TGCTGTCCCTGTGGGCTCACACGGGCACTGTGCACTCTACTCTGCGAGCATTCCTCATGGA 1932
Db      |||||||
Qy 604   TGCTGTCCCTGTGGGCTCACACGGGCACTGTGCACTCTACTCTGCGAGCATTCCTCATGGA 663
Db      |||||||
Qy 1933 ACAGCCTGACGCGCCAGGATGAAGGGCCAGACACGCGCCCTCGCTGAGACCAAGTCC 1992
Db      |||||||
Qy 664   ACAGCCTGACGCGCTCAGGATGAAGGGCCAGACACGCGCTCTGCTGAGACCAAGTCC 723
Db      |||||||
Qy 1993 AATCAGCCTTTCTTCCCGCAGGGTCCCTGTGATGGCTGAGAGGGTGTGGGTGCGCTCTTG 2052
Db      |||||||
Qy 724   AATCAGCCTTTCTTCCCGCAGGGTCCCTGTGATGGCTGAGAGGGTGTGGGTGCGCTCTTG 783
Db      |||||||
Qy 2053 ACCTACCTGAGACGAGTGGACACGACCTGTCTCAATTTAAACCCGGCTGACTCAGTGCA 2112
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Qy 784   ACCTACCTGAGACGAGTGGACACGACCTGTCTCAATTTAAACCCGGCTGACTCAGTGCA 843
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Qy 2113 GGGACGCGCCAGTGGTCCAGGGTCCAGGCTTCGCGCCCTCGCCAGGCTGTTCGGCTCACTG 2172
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Qy 844   GGGACGCGCTGCAAGTGGTCCAGGGTCCAGGCTTCGCGCCCTCGCCAGGCTGTTCGGCTCACTG 903
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Qy 2173 GGTGTGGCCTGGCTTCTGGGACAGGCACCATGCTGGGCGGGGTG 2217
Db      |||||||
Qy 904   GGTGTGGCCTGGCTTCTGGGACAGGCACCATGCTGGGCGGGGTG 948
Db      |||||||

RESULT 10
AL524358      949 bp      mRNA      linear      EST 22-MAY-2003
LOCUS      AL524358 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION      cDNA clone CS0DC06YB08 3-PRIME, mRNA sequence.
ACCESSION      AL524358
VERSION      AL524358.2 GI:31042619
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 949)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished
COMMENT      On Feb 13, 2001 this sequence version replaced gi:12787851.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster S245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC06DA04NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC06DA04NP1.

FEATURES
source
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/clone="CS0DC06YB08"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT      189 a   255 c   303 g   185 t   17 others
ORIGIN

Query Match      31.9%; Score 869.4; DB 9; Length 949;
Best Local Similarity 96.5%; Pred. No. 5.4e-178;
Matches 893; Conservative 13; Mismatches 17; Indels 2; Gaps 2;

Qy 1750 CCACACTGGAAGACGCCACCCACAGTGCCTCCACAGCGGCGGAGCCCTCTCGCC 1809
Db      |||||||
Qy 949   CAACACTGGAAGACGCCACCCACAGTGCCTCCACAGCGGCGGAGCCAA-SCYCTGGCC 891
Db      |||||||
Qy 1810 CCACCTGTGTGACATTTGGTGGGGCAAGCTGAGGGGGACCTACTCTCTCCCTCTCT 1869
Db      |||||||
Qy 890   CCACCTGTGTGACATTTGGTGGGGCAAGGCTGA-GGGGGACCTACTCTCTCTCTCTCT 832
Db      |||||||
Qy 1870 CCATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTCGAGCATCCCAT 1929
Db      |||||||
Qy 831   CCATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTCTACTCTCGAGCATCCCAT 772
Db      |||||||
Qy 1930 GGAACAGCCTTGACGCGCCAGGATGAAGGGGCCAGACACGCGCCCTCTGAGACACGG 1989
Db      |||||||
Qy 771   GGRACAGCCTTGATGCGCCAGGATGAAGGGGCCAGACCAACGCGCCCTGCTGAGACACGG 712
Db      |||||||
Qy 1990 TCCAATCCAGCCTTCTTCCCGCAGGGTCCCTGATGGCTGAGAGGGTGTGGGTGCCCTG 2049
Db      |||||||
Qy 711   TCCAATCCAGCCTTCTTCCCGCAGGGTCCCTGATGGCTGAGAGGGTGTGGGTGCCCTG 652
Db      |||||||
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QY 2512 GGAATTATTAGCAGCTTGGTCTCTGCGGTCGGGCGCAGCGCTGAACAGACCGGGGT 2571
Db 193 GGAATTATTAGCAGCTTGGTCTCTGCGGTCGGGCGCAGCGCTGAACAGACCGGGGT 134
QY 2572 GGAGTCAGGGCTGTCTTTCCGCGGTTCTGCGCACTTAGGAGTGTCCTTGGCGGGC 2631
Db 133 GGAGTCAGGGCTGTCTTTCCGCGGTTCTGCGCACTTAGGAGTGTCCTTGGCGGGC 74
QY 2632 CATTTACATTCCTGACCTCACTTTTCTCATCTCTATAAAACAGGCTGATGCCGTGCGGG 2691
Db 73 CNTNTACATTCCTGACCTMACATATCTCATCTGTATAAACAGGCTGATGCCGTGCGGG 14
QY 2692 CTAATGACCCAAAT 2704
Db 13 CTAATGACCCMAW 1

RESULT 12
AL525922 974 bp mRNA linear EST 23-MAY-2003
DEFINITION AL525922 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC015VF07 5-PRIME, mRNA sequence.
ACCESSION AL525922
VERSION AL525922.2 GI:31063786
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12789415.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC015CC04QP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC015CC04QP1.
FEATURES
source
Location/Qualifiers
1..974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC015VF07"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 199 a 310 c 278 g 183 t 4 others
ORIGIN
Query Match 31.4%; Score 855.6; DB 9; Length 974;
Best Local Similarity 98.8%; Pred. No. 5.4e-175;
Matches 869; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 37 GGGAGGAGCGCTTCATGTACAGCAGCAGGCGCATCTTCCTGGTCATCTGGTGCCG 96
Db 63 GGATGGAGCGCTTCATGTACAGCAGCAGGCGCATCTTCCTGGTCATCTGGTGCCG 122
QY 97 CACTGACGGGCTCGGCTCCCGTGAGAGCCCTCCCTCATCATCCCCCTGACCCGG 156
Db 123 CACTGACGGGCTCGGCKKCCCGTGAGAGCCCTCCCTCATCATCCCCCTGACCCGG 182
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QY 157 AGGGTCCCTGGAGCTCTCATGGAATGTACGTACACCCAGAGGCCATTCATTTCCAGC 216
Db 183 A-GGGTCCCTGGAGCTCTCATGGAATGTACGTACACCCAGAGGCCATTCATTTCCAGC 241
QY 217 TCCTGGTCGGAGGCTCAAGGCTGCGCTCTGTTTGGATGTCCGACCGTGCGAGCTTG 276
Db 242 TCCTGGTCGGAGGCTCAAGGCTGCGCTCTGTTTGGATGTCCGACCGTGCGAGCTTG 301
QY 277 AGAAGCAGAGATCTCTGGTGTCTGGACCGATGGGACACGTCTATTTTCGGACGCT 336
Db 302 AGAAGCAGAGATCTCTGGTGTCTGGACCGATGGGACACGTCTATTTTCGGACGCT 361
QY 337 GGAGTGACCAAGAGGGGCGAGATCCACTGGATCCCCAGCAGGACTACAGCTGTGCAGG 396
Db 362 GGAGTGACCAAGAGGGGCGAGATCCACTGGATCCCCAGCAGGACTACAGCTGTGCAGG 421
QY 397 TGCAGAGACCCCAAGAGGCTGACCTCTCTTTCAAGAGGCCCTTTGGACCTGCGACC 456
Db 422 TGCAGAGACCCCAAGAGGCTGACCTCTCTTTCAAGAGGCCCTTTGGACCTGCGACC 481
QY 457 CCAAGGATTACCTCATTTGAAGAGCGGCACTGTCCACTTTGGTCTACGGGATCCTGGAGG 516
Db 482 CCAAGGATTACCTCATTTGAAGAGCGGCACTGTCCACTTTGGTCTACGGGATCCTGGAGG 541
QY 517 CGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCTGCAGATGGGGCTGCAGAGGGTGC 576
Db 542 CGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCTGCAGATGGGGCTGCAGAGGGTGC 601
QY 577 AGCTTCCTGAAGCCCAATATCCCGAACCGAGTTGCCCTCAGACGCGTGCAACCATGAGG 636
Db 602 AGCTTCCTGAAGCCCAATATCCCGAACCGAGTTGCCCTCAGACGCGTGCAACCATGAGG 661
QY 637 TCCAAGCTCCCAATATCCAGATCCCGACCGAGGACCACTACTGTGTACATTAAGG 696
Db 662 TCCAAGCTCCCAATATCCAGATCCCGACCGAGGACCACTACTGTGTACATTAAGG 721
QY 697 AGCTTCCAAAGGGCTTCTCTCGGCACCACTATTAAGTACAGAGCCCATCTCACCAGG 756
Db 722 AGCTTCCAAAGGGCTTCTCTCGGCACCACTATTAAGTACAGAGCCCATCTCACCAGG 781
QY 757 GCAATGAGGCGCTTGTCCACACATGGAAGTCTTTCAGTGGCGCCCGAGATGACAGCG 816
Db 782 GCAATGAGGCGCTTGTCCACACATGGAAGTCTTTCAGTGGCGCCCGAGATGACAGCG 841
QY 817 TCCCCCACTTCAGCGGCGCTCGGACTCCAAGATGAACCCGACCGCTCAACTACTGCC 876
Db 842 TCCCCCACTTCAGCGGCGCTCGGACTCCAAGATGAACCCGACCGCTCAACTACTGCC 901
QY 877 GCCACGTGTGGCGCGCTGGGCGCTGGGTGCCAAGGCATT 916
Db 902 GCCACGTGTGGGCGCTGGGCGCTGGGTGCGATTT 941
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RESULT 13

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DEFINITION BX464421 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CS0DA004VB14 5-PRIME, mRNA sequence.
ACCESSION BX464421
VERSION BX464421.1 GI:31031625
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

88	QY	TGTTGGCCGCACTGCAGGGCTCGGCTCCCGTGAGAGCCCTCCCTATCATCATCCCC	147
59	Db	TGTTGGCCGCACTGCAGGGCTCGGCTCCCGTGAGAGCCCTCCCTATCATCATCCCC	118
148	QY	TGACCCGGAGGGTCCCTCGAGCTCTCATGGAAATGTCAGTACACCCAGAGGCCATCC	207
119	Db	TGACCCGGAGGGTCCCTCGAGCTCTCATGGAAATGTCAGTACACCCAGAGGCCATCY	178
208	QY	ATTTCAGCTCTGGTGCAGGAGCTCAAGCTCGCGTCTGTGGATGTCGAGCCGTG	267
179	Db	ATTTCAGCTCTGTGTCGAGGCTCAAGCTCGGNGTCTGTGGATGTCGAGCGTG	238
268	QY	GCAGCTTGAGAACGAGATCTCGTGGTCTCTGGACCGATGGGACATGCTCTATTTC	327
239	Db	GCAGCTTGAGAACGAGATTTGTGGTCTCTGGACCGATGGGACATGCTCTATTTC	298
328	QY	CGGACGCCTGGAGTGACCGAAGGGCGAGATCCACTGGATCCCGACGAGCATCACGC	387
299	Db	CGGACGCCTGGTGTACACAGAGGGCGAGATCCACTGGTTCCTCAGAGGATWCCGC	358
388	QY	TGCTGCAGCTGCAGAGGACCCAGAGGCTGACCTGCTCTTCAAGAGCCCTTTGGCA	447
359	Db	TGCTGCAGCTGCAGAGGATCTCAGAGGGCTGATCTGCTTTTMMAGGCCCTTTGGCA	418
448	QY	CCTCGACCCCCAAGGATTACCTATTGAAGACGGCACTGTCCACTTGGTCTACGGGATCC	507
419	Db	CCTCGACCCCCAGGWTTACCTATTGAGACGGCACTXTTCACTTGGTCTACGGGATCY	478
508	QY	TGAGGAGCCGTTCCGGTCACTGGAGGCCATCAACGGCTCGGGCTCTCAGATGGGCTGC	567
479	Db	TGAGGAGCCGTTCCGGTCACTGSMGGCCATCAACGGCTCGGGCTCTGCTGATGGGCTGC	538
568	QY	AGAGGCTGAGCTCTCTGAAGCCCAATATCCCCGAAACGGAGTTGCCCTCAGACGGGTGCA	627
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628	QY	CCATGGAGTCCAAGTCCCAATATCCAGATCCCCAGCCAGAGACCACTACTGGTGTCT	687
599	Db	CCATGGAGTCCAAGTCCCAATATCCAGATCCCCAGCCAGAGAMCACTGTCGTGTCT	658
688	QY	ACATTAAAGGAGCTTCCAAAGGCTCTCTCGGACCCCATTTATCAAGTACGAGCCATCG	747
659	Db	ACATTAAAGGAGCTTCCAAAGGCTCTCTCGGACCCCATTTATCAAGTACGAGCCATCG	718
748	QY	TCACCAAGGGCAATGAGGCCCTTTGCCACCATGGAAGTCTTTCAGTGGCCCCCGGAGA	807

Db	615	TGCTGGTCCATCCGGGAGATGTGCTCATCACCTCTCTGCAGGTACAAACAGCAAGACCGGG	674
Qy	1411	AGCTGGCCACAGTGGGGGCTTCGGGATCTCGGAGAGATGTGTCAACTAGTGCACCT	1470
Db	675	AGCTGGCCACAGTGGGGGCTTCGGGATCTCGGAGAGATGTGTCAACTAGTGCACCT	734
Qy	1471	ACTACCCCCAGAGCCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCGGCTTCTCTGCAGA	1530
Db	735	ACTACCCCCAGAGCCAGCTGGAGCTCTGCAAGACGGCTGTGGACGCCGGCTTCTCTGCAGA	794
Qy	1531	AGTACTTCCACCTCATCAACAGGTTCAACACGAGGATGTCTGCACCTGCCCTCAGCGGT	1590
Db	795	AGTACTTNCACCTCATCAACAGGTTCAACACGAGGATGTCTGCACCTGCCCTCAGCGGT	854
Qy	1591	CCGTGCTCAGCAGTTCCACC	1610
Db	855	CCGTGCTCAGCAGTTCCAAC	874
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LOCUS			
DEFINITION BQ068978 984 bp mRNA linear EST 02-APR-2002			
AGENCOURT_6740164 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802848			
5', mRNA sequence.			
ACCESSION BQ068978			
VERSION BQ068978.1 GI:19898024			
KEYWORDS EST.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE NIH-MGC http://mgi.nci.nih.gov/			
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT Unpublished			
Contact: Robert Strausberg, Ph.D.			
Email: cgabs-x@mail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Rubin Laboratory			
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNL at:			
http://image.llnl.gov			
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cloned into EcoRI/XhoI sites using the following 5'			
adaptor: GGCACGAG(G). Size-selected >500bp for average			
insert size 1.8kb. Library constructed by Ling Hong in			
the laboratory of Gerald M. Rubin (University of			
California, Berkeley) using ZAP-cDNA synthesis kit			
(Stratagene) and Superscript II RT (Life Technologies).			
Note: this is a NIH_MGC Library."			
BASE COUNT	189 a	339 c	281 g 175 t
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Query Match			
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Matches 870; Conservative 0; Mismatches 38; Indels 5; Gaps 3;			
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Qy	61	CAGCAGTGGCCATCTTCCTTGGTTCATCTCGTGGCGGCACATGCAGGGCTCGGCTCCCGTG	120
Db	64	CAGCAGTGGCCATCTTCCTTGGTTCATCTCGTGGCGGCACATGCAGGGCTCGGCTCCCGTG	123
Qy	121	AGAGCCCCCTCCCTATCATCATCCCCCTCGAACCCGAGGGGTCCTCTGGAGCTCTCATGGA	180
Db	124	AGAGCCCCCTCCCTATCATCATCCCCCTCGAACCCGAGGGGTCCTCTGGAGCTCTCATGGA	183
Qy	181	ATGTAGCTACACCCAGGAGGCATCCATTTTCCAGCTCTCTGTGCGAGGCTCAAGGCTG	240
Db	184	ATGTAGCTACACCCAGGAGGCATCCATTTTCCAGCTCTCTGTGCGAGGCTCAAGGCTG	243
Qy	241	GGTCTCTGTTGGGATGTCCGACCGTGGAGCTTGAGAACGAGATCTCGTGTGCTCT	300
Db	244	GGTCTCTGTTGGGATGTCCGACCGTGGAGCTTGAGAACGAGATCTCGTGTGCTCT	303
Qy	301	GGACCGATGGGACACTGCCTATTTTGGCGAGCGCTTGGAGTACACCAAGAGGGGCAGATCC	360
Db	304	GGACCGATGGGACACTGCCTATTTTGGCGAGCGCTTGGAGTACACCAAGAGGGGCAGATCC	363
Qy	361	ACTGTGATCCCGAGCAGGACTACAGCTCTGTCAGGTGAGAGGAGCCCGAGAGGCTGGA	420
Db	364	ACTGTGATCCCGAGCAGGACTACAGCTCTGTCAGGTGAGAGGAGCCCGAGAGGCTGGA	423
Qy	421	CCCTGCTTTTCAAGAGGCGCTTTGGCACCTGGACCCGACAGGATTAACCTCATTTGAAGCG	480
Db	424	CCCTGCTTTTCAAGAGGCGCTTTGGCACCTGGACCCGACAGGATTAACCTCATTTGAAGCG	483
Qy	481	GCACTCTCCACTTGGTCTACGGGATCCTGGAGGAGCGCTTCCGGTCACTGGAGGCCATCA	540
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Qy	541	ACGGTCTCGGCGCTGCAGATGGGGCTGCAGAGGTGCAGTCTCTGAAGCCCAATATCCCCG	600
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Qy	661	CCAGCCAGGAGACACGCTACTGCTGCTACATTAAGGAGCTTCCAAAGGGCTTCTCTCGGC	720
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Qy	721	ACACATTATCAAGTACAGGCCCATCGTCAACAGGGCAATGAGGCCCTTGTGCCACACA	780
Db	724	ACACATTATCAAGTACAGGCCCATCGTCAACAGGGCAATGAGGCCCTTGTGCCACACA	783
Qy	781	TGGAGTCTTCCAGTGGC-CCCCCGAGATGGACAGGT-CCCCCACTTCAGCGGGCCCTG	838
Db	784	TGGAGTCTTCCAGTGGC-CCCCCGAGATGGACAGGT-CCCCCACTTCAGCGGGCCCT	843
Qy	839	CG---ACTCCAAGATGAACCCGACCGCTCACTACTCTCCGCGCAATGCTGTGCGCCCTG	895
Db	844	GGGCACTCCAGGATGAACCCCGAACCCCGAACCCCGCTCACTACTCTCCGCGCAATGCTGTG	903
Qy	896	GGCCCTGGGTGCC	908
Db	904	GGCCCTGGGTGCC	916
RESULT 17			
BQ721360			
LOCUS			
DEFINITION BQ721360 943 bp mRNA linear EST 16-JUL-2002			
AGENCOURT_8291294 Lupski sympathetic_trunk Homo sapiens cDNA clone			
IMAGE:6194158 5', mRNA sequence.			
ACCESSION BQ721360			
VERSION BQ721360.1 GI:21860257			
KEYWORDS EST.			
SOURCE Homo sapiens (human)			
ORGANISM Homo sapiens			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 621.

FEATURES
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Location/Qualifiers

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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
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Directionally cloned using the following adaptors:

5'-TCGACCCACGGCTCG-3' and

5'-GACGAGTTCTAGTCGCGAGCGGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.9 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine); available through Life

Technologies."

BASE COUNT 199 a 324 c 252 g 166 t 2 others

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Best Local Similarity 98.0%; Pred. No. 1.8e-162;

Matches 839; Conservative 0; Mismatches 13; Indels 4; Gaps 3;

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Db 1 AGAGACCCCAAGAGGCTGACCTGCTTTTCAAGAGGCCCTTTGGCACCTGCGACCCCA 60

Qy 460 AGGATTACCTCATTTGAAGACGGCCTGTCCACTTTGGTCTACGGGATCCTGGAGGAGCGGT 519

Db 61 AGGATTACCTCATTTGAGAGGGCACTGTCCACTTTGGTCTACGGGATCCTGGAGGAGCGGT 120

Qy 520 TCCGGTCACTGGAGGCCATCAACGGCTCGGCCCTGCGAGTGGGGCTGAGAGGTGCGAGC 579

Db 121 TCCGGTCACTGGAGGCCATCAACGGCTCGGCCCTGCGAGTGGGGCTGAGAGGTGCGAGC 180

Qy 580 TCCTGAAGCCCAATATCCCGAACCGGAGTTGCCCTCAGAGCGCTGCACCATGAGGTCC 639

Db 181 TCCTGAAGCCCAATATCCCGAACCGGAGTTGCCCTCAGAGCGCTGCACCATGAGGTCC 240

Qy 640 AAGCTCCCAATATCCAGATCCCGACCGAGGAGCACCGTACTGTGTGTACATTAAAGGAGC 699

Db 241 AAGCTCCCAATATCCAGATCCCGACCGAGGAGCACCGTACTGTGTGTACATTAAAGGAGC 300

Qy 700 TTCCAAAGGGGTTCTCTCGGCACCAATATCAAGTACGAGGCCCATCGTCAACCAAGGGCA 759

Db 301 TTCCAAAGGGGTTCTCTCGGCACCAATATCAAGTACGAGGCCCATCGTCAACCAAGGGCA 360

Qy 760 ATGAGGCCCTTGTCCACACATGAAGTCTTCCAGTGGCCCCCGAGATGCACAGCGTCC 819

Db 361 ATGAGGCCCTTGTCCACACATGAAGTCTTCCAGTGGCCCCCGAGATGCACAGCGTCC 420

Qy 820 CCACCTTCAGCGGGCCCTGCGACTTCCAAGATGAAACCCGACCGGCTCAACTACTTGCGCC 879

Db 421 CCACCTTCAGCGGGCCCTGCGACTTCCAAGATGAAACCCGACCGGCTCAACTACTTGCGCC 480

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Db 481 ACGTGTGGCGCTGGCGCTGGTCCAGGCAATTTACTACCCAGAGGAGCGCGCC 540

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Db 721 TTCCACCACGGGAGACCGCTTTCATCTCTCACTGCTACTTGACCGAGC -AAGTGCACCCAG 780

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Db 841 GACTGGGAGAAAGGG 856

RESULT 18

LOCUS B0716251

DEFINITION AGENCOURT 8294403 Lupski_sympathetic_trunk Homo sapiens cDNA clone

INAMES: 6194209 5', mRNA sequence.

B0716251

ACCESSION B0716251

VERSION B0716251.1 GI:21855148

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 900)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 695.

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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:

NotI; Site_2: SalI; cDNA made by oligo-dT priming.


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Db 430 CTCAGCTCCACACACACTGACTGGGAGAAAGTGTCAAGTGTGTCTCGGGACGGCC 489
QY 1276 GGGAGTGGGAGATCGTGAACAGGACATCACTACAGCCCTCACTTCAGGAGATCCGCA 1335
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IMAGE:6189465_5', mRNA sequence.
ACCESSION BQ719089
VERSION BQ719089.1 GI:21857986
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lami.llnl.gov
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FEATURES

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Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACATAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies.
BASE COUNT 182 a 290 c 245 g 151 t 1 others
ORIGIN
Query Match 27.3%; Score 743; DB 13; Length 869;
Best Local Similarity 96.9%; Pred. No. 1.4e-150;
Matches 789; Conservative 0; Mismatches 21; Indels 4; Gaps 3;
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QY 750 ACCAAGGGCAATGAGGCCCTTGTCCACACATGGAAGTCTTCAGTGGCGCCCCGAGATG 809
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QY 930 GAGAGCGGCTTGGCTTCCGGGGTCCAGGGTCTCCAGATATCT-CCGCTTGGAGTTCA 988
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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Location/Qualifiers
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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 188 a 292 c 268 g 174 t
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QY 1009 TAGAGGACGAAACGACCTCCAGCATCTGCGATCTGTATACACCGCAAGTATCCACCAC 1068
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QY 1429 GCTTCGGGATCTGGAGGAGATGTGTCAACTACGTGCACTTACCCCCAGACGAGC 1488
Db 602 GCTTCGGGATCTGGAGGAGATGTGTCAACTACGTGCACTTACCCCCAGACGAGC 661
QY 1489 TGGAGCTCTGCAAGACCGGCTGTGGACGCGCGCTTCTTG-CAGAAAGTACTTCCACCTCATC 1547

Db 662 TGGAGCTCTGCAAGAGCGCTGTGGACGCGCGGTTCTGCCAAGTACTTCCAACTCCAT 721
QY 1548 AACAGGTTCAACAACGAGGATGTCTG-CACCTGCGCTCAGGCTCC----GTGTCTCAGC 1602
Db 722 CACCGGGTCTACAACGAGGATGTCTGTGGCTTGGGCTCAAGCGGTCCCGGGTGTCCAGCG 781
QY 1603 AGTTCACCTCTGTTCCCT--GGAACCTCTTCAACCGGACGCTACTGAAGGCCCTGTACAG 1660
Db 782 AGTTACCCCTGGTTCCTGGGACACACCTTTAACCGCGCGGGTTCGAAGGCCCTTTAA 841
QY 1661 CTTGCGGCCATCTCCATGC 1680
Db 842 GATTTCGGGCATACTCTGGC 861
RESULT 23
BX412000/c
BX412000/c
LOCUS
DEFINITION BX412000 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CSODA002YG07 3-PRIME, mRNA sequence.
ACCESSION BX412000
VERSION BX412000.1 GI:30649380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 947)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAK007CG02NM1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAK007CG02NM1.
FEATURES
source
1..947
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODA002YG07"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT 196 a 274 c 275 g 202 t
ORIGIN
Query Match 26.0%; Score 709.2; DB 13; Length 947;
Best Local Similarity 92.7%; Pred. No. 3e-143;
Matches 777; Conservative 0; Mismatches 58; Indels 3; Gaps 3;
QY 1859 CTCGCCCTCTCCATGTCCTCTGTTGGGTCAACCGGACATGTGCACTTACTTGC- 1917
Db 870 CTCGAACCTCTCCAGATGTTGTGCGGGAGTCCAATAGTCACTTGAATTTGACTCTGCG 811
QY 1918 GAGGATCCCATGACAGCCCTGCGCCCGAGATGAAGGGCCACACCGCCCTGC 1977
Db 810 GACATACCAATGGAAAACTCTGAAAAACCCAGGAAAGGGGGCAGACCCGACCTTGC 751
QY 1978 CTGAGACACGGTCCCAATCCAGCCTTCTTCCCCAGGGTCCCTTGCATGGCTGAGAGGCT 2037


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QY 1548 AACAGGTTCAACAAAGAGGATCTGCAC 1576
Db |||||||
720 AACAGGTTCAACAAAGAGGATCTGCAC 747

RESULT 25
BG683014
LOCUS 602651373F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:4761906 5',
DEFINITION mRNA sequence.
ACCESSION BG683014
VERSION BG683014.1 GI:13914411
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 905)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloned and distributed by: Incyte Genomics, Inc.
Cloned through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW615 row: b column: 19
High quality sequence stop: 698.
FEATURES
Location/Qualifiers
1..905
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/c clones="IMAGE:4761906"
/tissue type="neuroblastoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone.lib="NIH MGC 47"
/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGACAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene), and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 182 a 295 c 263 g 165 t
ORIGIN

Query Match 25.3%; Score 690.6; DB 10; Length 905;
Best Local Similarity 94.7%; Pred. NO. 3.2e-139;
Matches 791; Conservative 0; Mismatches 34; Indels 10; Gaps 7;

QY 1 TCAGTTCGTGGCGCAGCTGCGCGCCCGCCACATCGCGGAGCGACCTTCATGTACAGCA 60
Db |||||||
8 TCAGTTCGTGGCGCAGCTGCGCGCCCGCCACATCGCGGAGCGACCTTCATGTACAGCA 67

QY 61 CAGCAGTGGCCATCTTCTCGTTCATCTCTGTGGCGGCACTCAGGGGCTCGGCTCCCGGTG 120
Db |||||||
68 CAGCAGTGGCCATCTTCTCGTTCATCTCTGTGGCGGCACTCAGGGGCTCGGCTCCCGGTG 127

QY 121 AGAGCCCTCCCTATCAGATCCCGCTGGACCCGAGGGGTCTCGAGGCTTCATGGA 180
Db |||||||
128 AGAGCCCTCCCTATCAGATCCCGCTGGACCCGAGGGGTCTCGAGGCTTCATGGA 187

QY 181 ATGTGAGCTACACCCAGAGGCGCATCCATTTCCAGCTCTCGTGGGAGGCTCAAGCTG 240
Db |||||||
188 ATGTGAGCTACACCCAGAGGCGCATCCATTTCCAGCTCTCGTGGGAGGCTCAAGCTG 247

241 GC-GTCTGTTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCGAGATCTCGTGGTGTCTC 299
Db GCAGTCTCTGTTGGGATGTCCGACCGTGGCGAGCTTGAGAACGCGAGATCTCGTGGTGTCTC 307

QY 300 TGGACCGATGGGACACTGCTCTATTTTGGGACCGCTGGAGTGACCAAGAGGGGAGATC 359
Db |||||||
308 TGGACCGATGGGACACTGCTCTATTTTGGGACCGCTGGAGTGACCAAGAGGGGAGATC 367

QY 360 CACCTGTGATCCCCAG-CAGGACTACCGAGTCTCTGAGGTGCAGAGGAGCCCGAGAGGGCT 418
Db |||||||
368 CACCTGTGATCCCCAGAGAGACTACCGAGTCTCTGAGGTGCAGAGGAGCCCGAGAGGGCT 427

QY 419 GACCTGCTTTTCAAGAGGCGCTTTTGGCACTGCGACCCCAAGGATTAACCTCATTTGAAGA 478
Db |||||||
428 GACCTGCTTTTCAAGAGGCGCTTTTGGCACTGCGACCCCAAGGATTAACCTCATTTGAAGA 487

QY 479 CGGCACCTGTCACATGCTTACGGGATCCTGGAGAGCGCTTCGGTCTACTGGAGGCCAT 538
Db |||||||
488 CGGCACCTGTCACATGCTTACGGGATCCTGGAGAGCGCTTCGGTCTACTGGAGGCCAT 547

QY 539 -CAACGGGCTCGGGCTTCAGATGGGGTGCAGAGGGTGCAGCTCTCTGAAGCCCAATATCC 597
Db |||||||
548 CCAACGGGCTCGGGCTTCAGATGGGGTGCAGAGGGTGCAGCTCTCTGAAGCCCAATATCC 607

QY 598 CCGAACCGGAGTTGCCCTCAGACCGCTGCACCATGGAGGTCCAAAGTCCCAATATCCAGA 657
Db |||||||
608 CCGAACCGGAGTTGCCCTCAGACCGCTGCACCATGGAGGTCCAAAGTCCCAATATCCAGA 667

QY 658 TCCCCAGCCAGGAGACCACTGCTGCTGCTACATTA---GGAGCTTCCAAAGGGCTTCT 714
Db |||||||
668 TCCCCAGCCAGGAGAACCAAGTACTGCTGCTACATCGAAGGAGGCTTCCAAAGGGCTTCT 727

QY 715 CTCGGGACCACTATCAAGTACG-AGCCCATCTGC--ACCAAGGGCAATGAGGCCCTTG 771
Db |||||||
728 CTCGGGAGCAGCATTTCAAGTACGAAGCCCATCTCTCCACAGGCGCAAGTGAAGGCCCTTG 787

QY 772 T-CCACCACATGGAGTCTTCCAGTGGCGCCCGCCAGATGGACAGCGTCCCCCACT 825
Db |||||||
788 TACCACACATGGAGTCTTCCAGTGGCGCCCGCCAGATGGACAGCGTCCCCCACT 842

RESULT 26
AL525638/c
LOCUS AL525638 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DC012YJ10 3-PRIME, mRNA sequence.
ACCESSION AL525638
VERSION AL525638.2 GI:31063502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 808)
Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12789131.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster S245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC012DE05NP1&cluster=5245.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC012DE05NP1.
Location/Qualifiers
1..808
/organism="Homo sapiens"
FEATURES
source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC012XJ10"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Sma I
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 149 a 217 c 285 g 143 t 14 others
ORIGIN

Query Match 25.3%; Score 689; DB 9; Length 808;
Best Local Similarity 97.4%; Pred. No. 6.8e-139;
Matches 702; Conservative 7; Mismatches 10; Indels 2; Gaps 1;
QY 1693 CCTCAGCCCTCCGCTTCCAGGGTGAATGGAACCTGAGCCCTCGCCCAAGGTCACTCCA 1752
DB |||||
QY 721 CCTCAGCCCTCCGCTTCCAGAGTGAATGGAACCTGAGCCCTCGCCCAAGGTCACTCCA 662
DB |||||
QY 1753 CACTGGAAGAGCCCAACCCACACAGTGCCTCCACAGCAGGCGGAGAGCCCTGCTGCCCA 1812
DB |||||
QY 661 CACTGGAAGAGCCCAACCCACACAGTGCCTCCACAGCAGGCGGAGAGCCCTGCTGCCCA 602
DB |||||
QY 1813 CCGTTGTAGCATTTGTTGGGGCAAGGCTGAGGGGGAACCTACTCTCTCCCTCTCTCCA 1872
DB |||||
QY 601 CCGTTGTAGCATTTGTTGGGGCAAGGCTGAGGGGGAACCTACTCTCTCTCTCTCCA 542
DB |||||
QY 1873 TGCTGTCTCTGTGGCTCACACCGGCACTGCACTCTACTCTGAGAGATCCCATGGA 1932
DB |||||
QY 541 TGCTGTCTCTGTGGCTCACACCGGCACTGCACTCTACTCTGAGAGATCCCATGGA 482
DB |||||
QY 1933 ACAGCCCTGCACGCCAGGATGAAGGGCCAGACACAGCCCTCTGCTGAGACCAAGGTCC 1992
DB |||||
QY 481 ACAGCCCTGCATGCCAGGATGAAGGGCCAGACACAGCCCTCTGCTGAGACCAAGGTCC 422
DB |||||
QY 1993 AATCAGCCTTCTTCCCTCAGGCTCCCTGATGGCTGAGAGGTGTGGTGCCCTTTG 2052
DB |||||
QY 421 AATCAGCCTTCTTCCCTCAGGCTCCCTGATGGCTGAGAGGTGTGGTGCCCTTTG 362
DB |||||
QY 2053 ACCTACCTGGACCGAGTGGACCAAGCTCTGCTCCATTAAACCCGGCTGACTCAGTGCA 2112
DB |||||
QY 361 ACCTACCTGGACCGAGTGGACCAAGCTCTGCTCCATTAAACCCGGCTGACTCAGTGCA 302
DB |||||
QY 2113 GGGACAGCCCGACAGTGGTCCAGGGTCCAGCCCTCCCGCAGCCCTGTTCCGGCTCACTG 2172
DB |||||
QY 301 GGGACAGCCCGACAGTGGTCCAGGGTCCAGGGTCCCGCCCTCCCGCAGCCCTGTTCCGGCTCACTG 242
DB |||||
QY 2173 GGTGTGGCTGGCTTCTGGGACAGGACCATGCTGGGGCCGGGTGTGGAAATCAACGGGAA 2232
DB |||||
QY 241 GGTGTGGCTGGCTTCTGGGACAGGACCATGCTGGGGCCGGGTGTGGAAATCAACGGGAA 182
DB |||||
QY 2233 CGCCCCCGCCCCCGCTGCTCCCGGTGTGTCAGCGGGTGGGGTGGCGCTTAAACAT 2292
DB |||||
QY 181 CGCCCCCGCCCCCGCTGCTCCCGGTGTGTCAGCGGGTGGGGTGGCGCTTAAACAT 122
DB |||||
QY 2293 TTCCCTCTGAGTGGCTGCTGTTTTCAGTGGGGGCTTCCCTGCGAAGGAGGAGCC 2352
DB |||||
QY 121 TTCCCTCTGAGTGGCTGCTGTTTTCAGTGGGGGCTTCCCTGCGAAGGAGGAGCC 62
DB |||||
QY 2353 AGGCATTAGCTAGTTAGAGACTCGCTGGGAAATTGCTCCATTCTGAGTAAACAGATA 2412
DB |||||
QY 61 AGGCATTAGCTAGTTAGAGACTCGCTGG--AAATGCTCCATTMCNNWAAAWADATA 4
DB |||||
QY 2413 T 2413
DB 3 T 3

RESULT 27
BM013385
LOCUS
DEFINITION 603635129F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5434471 5',
EST 30-OCT-2001

mRNA sequence.
BM013385
BM013385.1 GI:16527739
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 916)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1911 row: j column: 08
High quality sequence stop: 696.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5434471"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 163 a 308 c 270 g 175 t
ORIGIN

Query Match 24.7%; Score 673.6; DB 12; Length 916;
Best Local Similarity 96.9%; Pred. No. 1.6e-135;
Matches 719; Conservative 0; Mismatches 19; Indels 4; Gaps 3;
QY 1691 GTCTTCAGCCCTCCGCTTCCAGGGTGAATGGAACCTGAGCCCTCGCCCAAGGTCACTC 1750
DB |||||
QY 1751 CACTGGAAGAGCCCAACCCACACAGTGCCTCCACAGCAGGCGGCGAAGCCCTGCTGGCCC 1810
DB |||||
QY 61 CACACTGGAAGAGCCCAACCCACACAGTGCCTCCACAGCAGGCGGCGAAGCCCTGCTGGCCC 120
DB |||||
QY 1811 CACCGTTCTCAGCATTTGTTGGGGCAAGAGCTGAGGGGGACCTACTCTCCCTCCCTCCTC 1870
DB |||||
QY 121 CACCGTTCTCAGCATTTGTTGGGGCAAGAGCTGAGGGGGACCTACTCTCCCTCCCTCCTC 180
DB |||||
QY 1871 CATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTTACTCTGCGAGCATCCCATG 1930
DB |||||
QY 181 CATGCTGTCCCTGTGGGCTCACACCGGCACTGTGCACTTACTCTGCGAGCATCCCATG 240
DB |||||
QY 1931 GAACAGCCCTGCAGCCCGCCAGGATGAAGGGGCCAGACACACCCCTGCTGAGACCAAGGT 1990
DB |||||
QY 241 GAACAGCCCTGCAGCCCGCCAGGATGAAGGGGCCAGACACACCCCTGCTGAGACCAAGGT 300
DB |||||
QY 1991 CCAATCCAGCCTTCTTCCCCCAGGGTCCCTGTCATGCTGAGAGGGTGTGGGTGCCCTGT 2050
DB |||||
QY 301 CCAATCCAGCCTTCTTCCCCCAGGGTCCCTGTCATGCTGAGAGGGTGTGGGTGCCCTGT 360
DB |||||
QY 2051 TGACCTTACCTGGACCGAGTGGACCAAGCCTCGTCCATTTAAACCCGGCTGACTCAGTG 2110
DB |||||

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Db 361 TGACCTACCTCGGACCGAGTGACACGACCTCGTCCATTTAAACCCGGCTGACTCAGTG 420
Qy 2111 CAGGACAGCCGACAGTGGTCCAGGCTCCAGCCCTCCGCGAGCCCTGTTCCGGCTCAC 2170
Db 421 CAGGACAGCTGACAGTGGTCCAGGCTCCAGCCCTCCGCGAGCCCTGTTCCGGCTCAC 480
Qy 2171 TGGGTGTGGCTGGCTTCTGGGACAGGACCATGCTGG-GCGGGGGTGTGGAATCACCGG 2229
Db 481 TGGGTGTGGCTGGCTTCTGGGACAGGACCATGCTGGTGGCGGGTGTGGAATCACCGG 540
Qy 2230 GAAGCCCGCCCGCCCGCCCGCTGCTCCCGGTGTGACGGGTGCGGGTCCCGTTAAA 2289
Db 541 GAAGCCCGCCCGCCCGCCCGCTGCTCCCGGTGTGACGGGTGCGGGTCCCGTTACA 600
Qy 2290 CATTTCCCTGCTGAGTGGCTGCTGTTTTCACAGTGGG--CGGCTTCCCTGCCAGCGAGG-C 2346
Db 601 CATTTCCCTGCTGAGTGGCTGCTGTTTTCACAGTGGGGGGTTCCTTGCACGAGGCC 660
Qy 2347 AGGACCGAGCAATTTAGCTAGTTAGAGACTCGCTGGGAAATTTGCTCCATTCTGAGTAAA 2406
Db 661 AGGACCGAGCAATTTAGCTAGTTAGAGACTCGCTGGGAAATTTGCTCCATTCTGAGTAAA 720
Qy 2407 CAGATATTTTCCGCCACCTAAA 2428
Db 721 CAGATATTTTCCGCCACCTAAA 742

RESULT 28
BF315987
LOCUS 601895945F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125395 5',
DEFINITION mRNA sequence.
ACCESSION BF315987
VERSION BF315987.1 GI:11264277
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE (bases 1 to 764)
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LUCM1013 row: 1 column: 12
High quality sequence stop: 719.
Location/Qualifiers
1. 764
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4125395"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
166 a 246 c 215 g 137 t

BASE COUNT
ORIGIN
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Query Match 24.7%; Score 672.8; DB 10; Length 764;
Best Local Similarity 96.9%; Pred. No. 2.2e-135;
Matches 729; Conservative 0; Mismatches 17; Indels 6; Gaps 4;

Qy 707 GGGTCTTCTCGGCAACACATTTAAAGTACGAGCCCATCTCAACAAAGGCAATGAGGC 766
Db 1 GGGTCTTCTCGGCAACACATTTAAAGTACGAGCCCATCTCAACAAAGGCAATGAGGC 60
Qy 767 CTTTGTCCACACATGGAAGTCTTCCAGTGGCGCCCGAGATGACAGGCTCCCACTT 826
Db 61 CTTTGTCCACACATGGAAGTCTTCCAGTGGCGCCCGAGATGACAGGCTCCCACTT 120
Qy 827 CAGCGGGCCCTTGGCACTCCAAAGATGAAACCCGACCGCTCAACTACTGCCGCCACGTGCT 886
Db 121 CAGCGGGCCCTTGGCACTCCAAAGATGAAACCCGACCGCTCAACTACTGCCGCCACGTGCT 180
Qy 887 GGCGCCCTGGGCGCTTGGTGCAGGCAATTTTATACCCAGAGGAAGCGGCGCTTGCCTT 946
Db 181 GGCGCCCTGGGCGCTTGGTGCAGGCAATTTTATACCCAGAGGAAGCGGCGCTTGCCTT 240
Qy 947 CGGGGGTCCAGGGTCTCCAGATATCTCGCTGGAGTTTCACTACCAACACCACTGGT 1006
Db 241 CGGGGGTCCA--GGTCTTCCAGATATCTCGCTGGAGTTTCACTACCAACACCACTGGT 299
Qy 1007 GATAGAGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACAGCAAGCTGCGGCG 1066
Db 300 GATAGAGGACGAAACGACTCCTCAGGCATCCGCTTGTACTACACAGCAAGCTGCGGCG 359
Qy 1067 CTTCAACCGGGGATCATGAGCTGGGACTGGTGTACACGCCAGTATGGCCATTCCACC 1126
Db 360 CTTCAACCGGGGATCATGAGCTGGGACTGGTGTACACGCCAGTATGGCCATTCCACC 419
Qy 1127 ACGGAGACCGCTTTCATCTCAGTGGTGTACACGCCAGTATGGCCATTCCACC 1186
Db 420 ACGGAGACCGCTTTCATCTCAGTGGTGTACACGCCAGTATGGCCATTCCACC 479
Qy 1187 GCCTCCCTCCGGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGACTGGGAGAA 1246
Db 480 GCCTCCCTCCGGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGACTGGGAGAA 539
Qy 1247 GGTGGTCAAGTGTCTGTCGGGACCGCGGAGTGGGAGATCGTG-AACAGGACAAATC 1305
Db 540 GGTGGTCAAGTGTCTGTCGGGACCGCGGAGTGGGAGATCGTGAAACAGGACAAATC 599
Qy 1306 ACTACAGCCCTCATTCCAGAGATCCGATGTTGAAGAGGTCGTGCGTCCATCCGG 1365
Db 600 ACTACAGCCCTCATTCCAGAGATCCGATGTTGAAGAGGTCGTGCGTCCATCCGG 659
Qy 1366 GAGATGTGCTCATCACCCTCTCGACGTTACAAACGGAAGACCGGAGTGGSCCAGTGG 1425
Db 660 GAGATGTGCTCATCA-CTCTGACAGTACAAACGGAAGAACGGGAGCTGG---CACAGG 715
Qy 1426 GGGGCTTCCGGGATCTCGAGGAGATGTGTGTC 1457
Db 716 GGGGCTTCCGGGATCTCGAGGAGAGTGTGTC 747

RESULT 29
BF315985
LOCUS 603634780F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5421955 5',
DEFINITION mRNA sequence.
ACCESSION BF315985
VERSION BF315985.1 GI:16525439
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Query Match 24.4%; Score 664.2; DB 10; Length 884;
Best Local Similarity 99.1%; Pred. No. 1.7e-133;


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Db      661 TCTTGGCTCTCAG---TCCACACACTGATGGAGACGGTGGCCCC 705
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LOCUS      AL525444 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION      cDNA clone CS0DC012YJ10 5-PRIME, mRNA sequence.
ACCESSION      AL525444
VERSION      AL525444
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12788937.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5245.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC012DE05QP1&cluster=5245.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CS0DC012DE05QP1.
FEATURES
Location/Qualifiers
1..817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC012YJ10"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/prime="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      157 a 257 c 240 g 154 t 9 others
ORIGIN
source
Query Match      23.3%; Score 633.8; DB 9; Length 817;
Best Local Similarity 99.5%; Pred. No. 64e-127;
Matches 646; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy      1 TCACTGCTGGCCAGAGCTGCGCGCCCGCCAGATGCGGGAGGAGCGCTTCATGTACAGCA 60
Db      75 TCACTGCTGGCCAGAGCTGCGCGCCCGCCAGATGCGGGAGGAGCGCTTCATGTACAGCA 134
Qy      61 CAGCAGTGGCCATCTTCTGTGATCTCTGTGCGCGCCAGCTGCGAGGCTGGCTCCCGTG 120
Db      135 CAGCAGTGGCCATCTTCTGTGATCTCTGTGCGCGCCAGCTGCGAGGCTGGCTCCCGTG 194
Qy      121 AGAGCCCTCTCCCTATFACATCCCTTGACCCCGGAGGGGTCCCTGGAGCTCTCATGGA 180
Db      195 AGAGCCCTCTCCCTATFACATCCCTTGACCCCGGAGGGGTCCCTGGAGCTCTCATGGA 253
Qy      181 ATGTACAGTACACCCAGAGGCGCATCCATTTCCAGCTCTCTGTGCGGAGGCTCAAGGCTG 240
Db      254 ATGTACAGTACACCCAGAGGCGCATCCATTTCCAGCTCTCTGTGCGGAGGCTCAAGGCTG 313
Qy      241 GCCTCTGTTTGGATGTGCGACCGTGGCGAGCTTGAGAACCGAGATCTCGGTGGTCTCT 300
Db      314 GCCTCTGTTTGGATGTGCGACCGTGGCGAGCTTGAGAACCGAGATCTCGGTGGTCTCT 373
Qy      301 GGACCGATGGGACATGCTGCTATTTTGGCGAGCGCTGAGTGAACGAGAGGGGAGATCC 360
|||||
Db      374 GGACCGATGGGAGCACTGCGCTATTTTGGGACGCTGAGTGACCAAGGGGAGATCC 433
Qy      361 ACCTGGATCCCGACAGGAGCTACAGCTGTGTGAGGTGTCAGAGGAGCCCGAGAGGCTGA 420
Db      434 ACCTGGATCCCGACAGGAGCTACAGCTGTGTGAGGTGTCAGAGGAGCCCGAGAGGCTGA 493
Qy      421 CCCTGCTTTTCAAGAGGCGCTTTTGGCACCTCCGACCCAGAGGATTACCTCATTTGAGAGC 480
Db      494 CCCTGCTTTTCAAGAGGCGCTTTTGGCACCTCCGACCCAGAGGATTACCTCATTTGAGAGC 553
Qy      481 GCACGTGTCACCTTGGTCTACGGGATCCTGGAGGAGCGGTTCCCGTCACTGGAGGCCATCA 540
Db      554 GCACGTGTCACCTTGGTCTACGGGATCCTGGAGGAGCGGTTCCCGTCACTGGAGGCCATCA 613
Qy      541 ACGGCTCGGCGCTGCAGATGGGCTGCAGAGGGTGCAGCTCTCTGAAGCCCAATATCCCCG 600
Db      614 ACGGCTCGGCGCTGCAGATGGGCTGCAGAGGGTGCAGCTCTCTGAAGCCCAATATCCCCG 673
Qy      601 AACCGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGTCCCA 649
Db      674 AACCGAGTTGCCCTCAGACGCGTGCACCATGGAGGTCCAAGTCCCA 722
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RESULT 33
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LOCUS      601897245F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126571 5',
DEFINITION      mRNA sequence.
ACCESSION      BF311746
VERSION      BF311746.1 GI:11259506
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW1016 row: j column: 12
High quality sequence stop: 732.
FEATURES
Location/Qualifiers
1..945
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126571"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/notes="Organ: brain; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      207 a 300 c 277 g 161 t
ORIGIN
source
Query Match      23.2%; Score 633; DB 10; Length 945;
Best Local Similarity 90.8%; Pred. No. 1e-126;
Matches 767; Conservative 0; Mismatches 60; Indels 18; Gaps 8;

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QY 707 GGGCTTCTCTCGGCACCACTATCAAGTACGAGCCCATCGTCACCAAGGCAATGAGGC 766
Db 1 GGGCTTCTCTCGGCACCACTATCAAGTACGAGCCCATCGTCACCAAGGCAATGAGGC 60
QY 767 CTTTGTCCACCATGGAAGTCTTCAGTGGCGCCCGAGATGGACAGGCTCCCACTT 826
Db 61 CTTTGTCCACCATGGAAGTCTTCAGTGGCGCCCGAGATGGACAGGCTCCCACTT 120
QY 827 CAGCGGGCCCTCGACTCAAGATGAACCCGACCGCTCAACTACTGCGCCAGCTGT 886
Db 121 CAGCGGGCCCTCGACTCAAGATGAACCCGACCGCTCAACTACTGCGCCAGCTGT 180
QY 887 GCGCCCTTGGGCTTGGTGGCAAGGCATTTTACTACCCAGAGGAGCGGCTTGGCTT 946
Db 181 GCGCCCTTGGGCTTGGTGGCAAGGCATTTTACTACCCAGAGGAGCGGCTTGGCTT 240
QY 947 CCGGGGTTCAGGGTCTTCAGATATCTCGGCTTGAAGTTCTACTACCAACCACTGGT 1006
Db 241 CCGGGGTTCAGGGTCTTCAGATATCTCGGCTTGAAGTTCTACTACCAACCACTGGT 299
QY 1007 GATAGAAGGACGAAACGACTCTCAGGATCGCTTGTACTACAGACCAAGCTGCGGC 1066
Db 300 GATAGAAGGACGAAACGACTCTCAGGATCGCTTGTACTACAGACCAAGCTGCGGC 359
QY 1067 TTCAACCGGGGATCATGGAGCTGGGACTGGTGTACACGCGAGTGATGGCCATTCACC 1126
Db 360 TTCAACCGGGGATCATGGAGCTGGGACTGGTGTACACGCGAGTGATGGCCATTCACC 419
QY 1127 ACGGAGACCGCTTCACTCTCAGTCTGCTACTGACGAGCAAGTGACCCAGCTGGCACT 1186
Db 420 ACGGAGACCGCTTCACTCTCAGTCTGCTACTGACGAGCAAGTGACCCAGCTGGCACT 479
QY 1187 GCCTCCCTCCGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGACTGGAGAA 1246
Db 480 GCCTCCCTCCGGATCCACATCTTCGCTCTCAGCTCCACACACACCTGACTGGAGAA 538
QY 1247 GGTGTACAGTGTGTGTCGGGAGCGCGGAGTGGGAGATCGTGAAACCAAGCAATCA 1306
Db 539 GGTGTACAGTGTGTGTCGGGAGCGCGGAGTGGGAGATCGTGAAACCAAGCAATCA 598
QY 1307 CTACAGCCCTCACTTCCAGGAGATCC-GCATGTTGAAGAAGTGTGTCGTCATCCGG 1365
Db 599 CTACAGCCCTCACTTCCAGGAGATCCGGCATGTTGAAGAAGTGTGTCGTCATCCGG 658
QY 1366 GAGATG-----TGCTCATACCTCTGACGTACACACCGRA-GACCGGAGCTGG- 1416
Db 659 GGGAGATGTGCTCATCAACTCTCTGGCAGCTACACACCGRAAGGAGCGGAGCTGG 718
QY 1417 -CCAGTGGGGGCTTCGGGATCCTG---GAGGAGATGTGTCAACTAGCT--GCACT 1470
Db 719 CCACAGTGGGGGCTTCGGGATCCTGGAGGAGATGGGGTGTCCACTAAGTTGCATA 778
QY 1471 ACTACCCCAAGCGAGCTGAGCTGTGCAAGACGGCTGTGGAAGCGCGCTTCTGACGA 1530
Db 779 ATTACCCCAAGAAAGCAGTGGAGGTCTGGAAGAGCGGGAAGCGCGTCCCGAAAGT 838
QY 1531 AGTAC 1535
Db 839 ATTCC 843
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RESULT 34
LOCUS BF316475
DEFINITION BF316475 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131041 5',
mRNA sequence.
ACCESSION BF316475
VERSION BF316475.1 GI:11264832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 759)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM1028 row: d column: 18
High quality sequence stop: 670.
FEATURES
Location/Qualifiers
1..759
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/db_xref="taxon:9606"
/clone="IMAGE:4131041"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: Brain; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
BASE COUNT 165 a 253 c 204 g 137 t
ORIGIN
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Query Match 23.2%; Score 631.8; DB 10; Length 759;
Best Local Similarity 96.0%; Pred. No. 1.7e-126;
Matches 723; Conservative 0; Mismatches 22; Indels 8; Gaps 7;
QY 530 GGAGGCCATCAACGGCTCGGGCTCGAGATGGGCTGCGAGGGTGCAGCTCTTGAAGCC 589
Db 2 GGAGGCCATCAACGGCTCGGGCTCGAGATGGGCTGCGAGGGTGCAGCTCTTGAAGCC 61
QY 590 CAATATATCCCAAGCCGAGTGTCCCTCAGACGCGTGACCATGGAGTCCCAAGCTCCCAA 649
Db 62 CAATATATCCCAAGCCGAGTGTCCCTCAGACGCGTGACCATGGAGTCCCAAGCTCCCAA 121
QY 650 TATCCAGATCCCAAGCCGAGGAGACCATGTACTGTGTCTACATTAA-GGAGCTTCCAAAG 708
Db 122 TATCCAGATCCCAAGCCGAGGAGACCATGTACTGTGTCTACATTAAAGCGAGCTTCCAAAG 181
QY 709 GCTTCTCTCGCACCATATTAAGTACGAGCCCATCGTCCAGAGGGCAATGAGGCC 768
Db 182 GCTTCTCTCGCACCATATTAAGTACGAGCCCATCGTCCAGAGGGCAATGAGGCC 241
QY 769 TTGTCCACCATGGAAGTCTTCCAGTGGCGCCCGGAGATGGACA-GGGTCCCGCCTTC 827
Db 242 TTGTCCACCATGGAAGTCTTCCAGTGGCGCCCGGAGATGGACAATGTGTCCCGCCTTC 301
QY 828 AGC--GGGCGCTGCGACTCCCAAGATGAACCC-GACCGCTTCAACTACTGCGCCACGTG 884
Db 302 AGCTGGTGGCTGGACTCCCAAGATGAACCCCTGACCGCTTCAACTACTGCGCCACGTG 361
QY 885 CTGGCGCGCTGGGCGCTTGGTGGCGGATTTTACTACCCAGAGGAAGCGGCTTGGC 944
Db 362 CTGGCGCGCTGGGCGCTTGGTGGCGGATTTTACTACCCAGAGGAAGCGGCTTGGC 421
QY 945 TTGGGGGTTCAGGGTCTTCCAGATATCTCGGCTGGAAGTTTCACTACCAACCCACTG 1004
Db 422 TTGGGGGTTCAGGGTCTTCCAGATATCTCGGCTGGAAGTTTCACTACCAACCCACTG 481
QY 1005 GTGATAGA-AGGAGCAAAACGACTCTCTCAGGATCCGCTTGTACTACAGCAAGCTGCG 1063
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Db      482 GTGATAGACGAGCAAGAAACGACTCTCTCAGGCATCGCTTGACTACACAGCCAGCTGGC 541
QY      1064 GCGCTTCAACGGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTATGCCATTTC 1123
Db      542 GCGCTTCAACGGGGGATCATGGAGCTGGGACTGGTGTACACGCCAGTATGCCATTTC 601
QY      1124 ACCAGGGAGACCGCTTCATCTCTCACTGGCTACTGACGAGCAAGTGCACCCAGCTGGC 1183
Db      602 ACCAGGGAGACCGCTTCATCTCTCACTGGCTACTGACGAGCAAGTGCACCCAGCTGGC 661
QY      1184 ACTGCTCCCTCCGGGATCCACATCTTGGCTCTCAGCTCCACACACACCTGACTGGGAG 1243
Db      662 ACTGGCTCCCTCCGGGATCACATCTTCG-CTCAGCTCACACACACCTTGACTGGGAG 720
QY      1244 AAAGTGGTACAGTGTCTGTCGGGACGCCG 1276
Db      721 AACGGTGGAC-CAGTGTGTCTCCGGAGCCCG 752

RESULT 35
LOCUS   BX411774/c
DEFINITION BX411774 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ACCESSION BX411774
VERSION   BX411774
KEYWORDS  BX411774.1 GI:30763182
SOURCE   EST.
ORGANISM Homo sapiens (human)
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL  1 (bases 1 to 908)
COMMENT  Full-length cDNA libraries and normalization
        Unpublished
        Contact: Genoscope
        Genoscope - Centre National de Sequencage
        Bp 191 91006 EVRY cedex - France
        Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
        Library was constructed by Life Technologies, a division of
        Invitrogen. This sequence belongs to sequence cluster 5245.f For
        more information about this cluster, see
        http://www.genoscope.cns.fr/
        cgi-bin/cluster.cgi?seq=CS0BAK003CA12NM1&cluster=5245.f. Contact :
        Feng Liang Email : fliang@lifetech.com URL :
        http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
        Faraday Avenue Genoscope sequence ID : CS0BAK003CA12NM1.
        Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="Cl0BB0112C07"
            /tissue_type="NEUROBLASTOMA"
            /note="Vector; pCMVSPORT 6; 1st strand cDNA was primed
            with a NotI-oligo(dT) primer. Five prime end enriched,
            double-strand cDNA was digested with Not I and cloned into
            the Not I and EcoRV sites of the pCMVSPORT 6 vector.
            Library was not normalized."
            BASE COUNT 172 a 267 c 253 g 216 t
            ORIGIN
              Query Match 22.8%; Score 621.4; DB 13; Length 908;
              Best Local Similarity 91.0%; Pred. No. 3.2e-124;
              Matches 694; Conservative 0; Mismatches 66; Indels 3; Gaps 3;

QY      1935 AGCCTGCAGCCGAGATGAAGGGCCAGACACCGCCCTGCTGAGACCAAGTCCAA 1994
Db      766 AGCAAGACACAGCGGACCGGAAAGGAAAAAACAACACATCGTTAAACAGCGGACAA 707
QY      1995 TCCAGCGCTTCTCCCGCAGGGTCCCTGCATCGCTGAGAGGTGTGGGTGCCTTTGCAC 2054

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Db      706 TACAAACTTCTTCCACAGGGTCCCTCGCATGAAGGAGAAGTGATGAGTACCTTATTACA 647
QY      2055 CTACCTTGAGCC-GAGTGGACACGACCTCGTCAATTAAACCCGGCTGACTCAGTGCAG 2113
Db      646 CAACCTTGAGCCGAGTGGGCGCAGGGCTCGTCAATTAAACCCAGGCTGACTCAGTGCAG 587
QY      2114 GGACAGCCCGCACAGTGTGTCAGGGTCCAGCCCTCCGCCAGCCCTGTTCGCCCTCACTGG 2173
Db      586 GGAAGAGCTGCACA-TGGTCCAGGGTCCAGCCCTCCGCCAACCCCTGTTCGCCCTCACTGG 528
QY      2174 GTGTGGCTGGCTTCTGGGACAGGCACCATGCTGGGCGGGGTGTGGAATCACCGGGAAC 2233
Db      527 GTGTGGCTGGCTTCTGGGACAGGCACCATGCTGGGCGGGGTGTGGAATCACCGGGAAC 468
QY      2234 GCCCGCCGCCCGCCCGCTGCTCCCGGTGTGACGGGGTGGGGTGCCTTTAAACATT 2293
Db      467 GCACACCGCCCGGAAACCGCTGCTCCCGGTGTGACAGGGTGGCGGTGCGGCTTAAACATT 408
QY      2294 TCCTGCTGAGTGGCTCGTGTTCACAGTGGGGCGGCTTCCCTGCGACGAGGAGGACCA 2353
Db      407 TCCTGCTGAGTGGCTCGTGTTCACAGTGGGGCGGCTTCCCTGCGACGAGGAGGACCA 348
QY      2354 GGCATTAGCTAGTGTAGAGACTCGCTGGGAATTTGCTCCATTTCCTGAGTAAACAGATAT 2413
Db      347 GGCATTAGCTAGTGTAGAGACTCGCTGGGAATTTGCTCCATTTCCTGAGTAAACAGATAT 288
QY      2414 TTTGCGCCACCTAAAGGGAAGCCCTGACAAACATATACCAAAAGACAGCGGCGCAAG 2473
Db      287 TTTGCGCCACCTAAAGGGAAGCCCTGACAAACATATACCAAAAGACAGCGGCGCAAG 228
QY      2474 ATCCAGCGGGGCTTTGGGCGCGGTTCCAGTGGGGTGGAAATTATTAGCACCACTTGC 2533
Db      227 ATCCAGCGGGGCTTTGGGCGCGGTTCCAGTGGGGTGGAAATTATTAGCACCACTTGC 168
QY      2534 TTCTCTGCGGTGGGCGCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGTTCCG 2593
Db      167 TTCTCTGCGGTGGGCGCAGCGCTGAACAGACCGGGGTGGAGTCAGGGCTGTGTTCCG 108
QY      2594 CTGTGTTTCGCACCTTAGGGAGTGTGCTTGGGGGGGCATTTCACATTCTCTGACCTCA 2653
Db      107 CGTGTGTTCTGCACCTTAGGGAGTGTGCTTGGGGGGGCATTTCACATTCTCTGACCTCA 48
QY      2654 CTTTCTCATCTGTAAACACAGGCTGATGCCGTGGGCTTAAT 2696
Db      47 CTTTCTCATCTGT-AAACACAGGCTGATGCCGTGGGCTTAAT 6

RESULT 36
LOCUS   BF206759
DEFINITION 601871147F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101706 5',
ACCESSION BF206759
VERSION   BF206759.1 GI:11100345
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL  1 (bases 1 to 769)
COMMENT  NIH-MGC http://mgs.nci.nih.gov/.
        National Institutes of Health, Mammalian Gene Collection (MGC)
        Contact: Robert Strausberg, Ph.D.
        Email: sgabbs-r@mail.nih.gov
        Tissue Procurement: ATCC
        cDNA Library Preparation: Ling Hong/Rubin Laboratory
        DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
        plate: LLCW973 row: n column: 11
        High quality sequence stop: 720.

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Db 718 --GGGTGGGGTCAGGGCTGGGC-TTCCGGTGGTCTGCACCTTAGGAGTGTG 766

RESULT 37
BI195352
LOCUS
DEFINITION
602944718F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:5092565 5', mRNA sequence.
626 bp mRNA linear EST 10-JUL-2001

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BI195352
BI195352.1 GI:14650372
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 626)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LNCMI958 row: d column: 06
High quality sequence stop: 626.
Location/Qualifiers
1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5092565"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 133 a 199 c 182 g 112 t
ORIGIN

Query Match 22.1%; Score 601.4; DB 12; Length 626;
Best Local Similarity 99.5%; Pred. No. 6.2e-120;
Matches 624; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 829 GCGGGCCCTGGGACTCCAAAGATGAACCCGACCGCTCAACTACTCGCGCCACAGTGTCTGG 898
DB 2 GCGGGCCCTGGGACTCCAAAGATGAACCCGACCGCTCAACTACTCGCGCCACAGTGTCTGG 61
QY 899 CCGCTTGGGCGCTGGTGGTCCCAAGGCATTTTACTACCCAGAGGAAGCGGCTTTCCTTCG 948
DB 62 CCGCTTGGGCGCTGGTGGTCCCAAGGCATTTTACTACCCAGAGGAAGCGGCTTTCCTTCG 121
QY 949 GGGGTCCAGGGTCTCCAGATATCTCCGCTGGAGTTTCACTACCAACCCACCTGGTGA 1008
DB 122 GGGGTCCCA-GGTCTCCAGATATCTCCGCTGGAGTTTCACTACCAACCCACCTGGTGA 180
QY 1009 TAGAGGACGAAACGACTCTCTCAGGCATCCGCTTGTACTACAGCCCAAGCTCGGCGCT 1068
DB 181 TAGAGGACGAAACGACTCTCTCAGGCATCCGCTTGTACTACAGCCCAAGCTCGGCGCT 240
QY 1069 TCACCGGGGATCATGAGCTGGGACTGTGTACAGCCAGTGTAGTGTGATGGCCATTCCACCAC 1128
DB 241 TCACCGGGGATCATGAGCTGGGACTGTGTACAGCCAGTGTAGTGTGATGGCCATTCCACCAC 300

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4101706"
/tissue_type="neuroblastoma"
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/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 134 a 244 c 239 g 152 t
ORIGIN

Query Match 22.7%; Score 619.2; DB 10; Length 769;
Best Local Similarity 95.3%; Pred. No. 9.2e-124;
Matches 736; Conservative 0; Mismatches 23; Indels 13; Gaps 9;

QY 1846 GGGGGACTACTCTCCCTCTCTCATGCTGTCTGTGGCTCACACCGGACTGTGC 1905
DB 8 GGGGGACTACTCTCCCTCTCTCATGCTGTCTGTGGCTCACACCGGACTGTGC 67
QY 1906 ACTTACTCTGCACCATCCCATGGAACAGCCCTGCAGCCCGAGGATGAAGGGCCAGA 1965
DB 68 ACTTACTCTGCACCATCCCATGGAACAGCCCTGCAGCCCGAGGATGAAGGGCCAGA 127
QY 1966 CCACGGCCCTGCTGAGACACCGGTCCAAATCCAGCGCTTCTTCCCGCCGCTCCCTGCAT 2025
DB 128 CCACGGCCCTGCTGAGACACCGGTCCAAATCCAGCGCTTCTTCCCGCCGCTCCCTGCAT 187
QY 2026 GCGTGAGAGGTGTGGGTGCTTGTACCTACCTGACGAGTGGACACGACCTCGT 2085
DB 188 GCGTGAGAGGTGTGGGTGCTTGTACCTACCTGACGAGTGGACACGACCTCGT 246
QY 2086 CCATTAAACCGGCTGACTCAGTCGAGGACAGCCGACAGTGTTCAGGTTCCAGCC 2145
DB 247 CCATTAAACCGGCTGACTCAGTCGAGGACAGCCGACAGTGTTCCTCA-GTCCAGCC 305
QY 2146 CTCGGCAGCCCTGTTCGCCCTCACTGGGTGTGGCTGGCTTCTGGACAGGACCAATGC 2205
DB 306 CTCGGCAGCCCTGTTCGCCCTCACTGGGTGTGGCTGGCTTCTGGACAGGACCAATGC 365
QY 2206 TGGGCGGGGTGTGGAATCACCGGAAACGCCCCCGCCCGCTGTCTCCGGTGTG 2265
DB 366 TGGGCGGGGTGTGGAATCACCGGAAACGCCCCCGCCCGCTGTCTCCGGTGTG 425
QY 2266 CAGCGGTGGGGTGGGCTTAAACATTTCCCTGTGAGTGGCTGTGTTCACAGTGG 2325
DB 426 CAGCGGTGGGGTGGGCTTAAACATTTCCCTGTGAGTGGCTGTGTTCACAGTGG 485
QY 2326 CGGCTTCCCTGCGACGAGGACAGGACATTTAGTCTAGTGTAGAGACTCGCTCGGAA 2385
DB 486 CGGCTTCCCTGCGACGAGGACAGGACATTTAGTCTAGTGTAGAGACTCGCTCGGAA 544
QY 2386 ATTGTCCATTCTGAGTAAACAGATATTTTTCGCCACCTAAAGGGAAGCCCTGACAA 2445
DB 545 ATTGTCCATTCTGAGTAAACAGATATTTTTCGCCACCTAAAGGGAAGCCCTGACAA 604
QY 2446 ACTATACCAAGACGAGCGGCAAGATCCAGCGGGCTTCTGGGCGCGGTTCCAGC 2505
DB 605 A-TATACCAAGACGAGCGG- AAGATCCAGCGGGCTTCTGGGCG-CGGTTCACG 661
QY 2506 TGGGTGGAAATTATTAGCACACGCTTGTCTCTCTCGGTCGGGCGACGCGCTGAACAGAC 2565
DB 662 TGGGTGGAAATTATTAGCACCA ----GTGTCTCTCGGTCGGGCGACGCTGAACAGAC 717
QY 2566 CCGGGTGGAGTCAGGCTGTGCTTTCGCGTGGTTCTGCACTTAGGAGGTG 2617

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QY      1129 GGGAGCCGCTTCATCTCCTCACTGGCTACTGACCGGACAAAGTGACCCAGCTGGCACTGC 1188
Db      |||||||
QY      301 GGGAGCCGCTTCATCTCCTCACTGGCTACTGACCGGACAAAGTGACCCAGCTGGCACTGC 360
Db      |||||||
QY      1189 CTCCTCCGGGATCCACATCTTCGCTCTCACTCTCCACACACACTGACTGGGAGAAAGG 1248
Db      |||||||
QY      361 CTCCTCCGGGATCCACATCTTCGCTCTCACTCTCCACACACACTGACTGGGAGAAAGG 420
Db      |||||||
QY      1249 TGGTCACTGCTGGTCCGGGACGGCCGGGAGTGGGAGATCGTGAACACGAGACATCACT 1308
Db      |||||||
QY      421 TGGTCACTGCTGGTCCGGGACGGCCGGGAGTGGGAGATCGTGAACACGAGACATCACT 480
Db      |||||||
QY      1309 ACAGCCCTCCTTCAGGAGATCCGATGTTGAAGAGTCTGTCGCTCCATCCGGGAG 1368
Db      |||||||
QY      481 ACAGCCCTCCTTCAGGAGATCCGATGTTGAAGAGTCTGTCGCTCCATCCGGGAG 540
Db      |||||||
QY      1369 ATGTGCTCATCTTCCTGCGACGACACACGGAAGACCGGAGTGGCCACAGTGGGG 1428
Db      |||||||
QY      541 ATGTGCTCATCTTCCTGCGACGACACACGGAAGACCGGAGTGGGAGTGGGAGTGGG 599
Db      |||||||
QY      1429 GTTCCGGGATCCTGGAGGAGATGTG 1455
Db      |||||||
QY      600 GTTCCGGGATCCTGGAGGAGATGTG 626

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LOCUS      601150168F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502889 5',
DEFINITION mRNA sequence.
ACCESSION BE260752
VERSION   BE260752.1 GI:9132302
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM175 row: g column: 18
High quality sequence stop: 598.
Location/Qualifiers
1. 605
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:3502889"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
119 a 213 c 159 g 114 t
BASE COUNT 22.0%; Score 599.2; DB 10; Length 605;
ORIGIN
Query Match

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Best Local Similarity 99.5%; Pred. No. 1.8e-119;
Matches 601; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1344 AAGGTCGCTGGTCCATCCGGGAGATGTGCTATCACTCTCTGCACTGCAACACCGAA 1403
Db      |||||||
QY      1  AAGGTCGCTGGTCCATCCGGGAGATGTGCTATCACTCTCTGCACTGCAACACCGAA 60
Db      |||||||
QY      1404 GACCGGAGCTGGCCACAGTGGGGGGTTCGGGATCCTGGAGAGATGTGTGTCAACTAC 1463
Db      |||||||
QY      61  GACCGGAGCTGGCCACAGTGGGGGGTTCGGGATCCTGGAGAGATGTGTGTCAACTAC 120
Db      |||||||
QY      1464 GTGCACTACTACCCCGACAGCGAGCTGGAGCTCTGCAAGAGCGCTGTGAGCGCGGCTTC 1523
Db      |||||||
QY      121  GTGCACTACTACCCCGACAGCGAGCTGGAGCTCTGCAAGAGCGCTGTGAGCGCGGCTTC 180
Db      |||||||
QY      1524 CTGCAAGAGTACTTCCACCTCATCAACAGGTTCAACAGGATGTCTGCACTCTGCCCT 1583
Db      |||||||
QY      181  CTGCAAGAGTACTTCCACCTCATCAACAGGTTCAACAGGATGTCTGCACTCTGCCCT 240
Db      |||||||
QY      1584 CAGCGCTCCGTGTCTCAGCAGTTCACTCTGTTCCTGGAACTCTTCAACCGGACGTA 1643
Db      |||||||
QY      241  CAGCGTCCGTGTCTCAGCAGTTCACTCTGTTCCTGGAACTCTTCAACCGGACGTA 300
Db      |||||||
QY      1644 CTGAAGGCCCTGTACAGCTTCGCGCCATCTCCAGCTTCGAGCGCTGCAACAGTCTCTAGCCGTC 1703
Db      |||||||
QY      301  CTGAAGGCCCTGTACAGCTTCGCGCCATCTCCAGCTTCGAGCGCTGCAACAGTCTCTAGCCGTC 360
Db      |||||||
QY      1704 CGCTTCCAGGGTGAATGGAACTTGAGCCCTGCGCCAAAGGTCATCTCCACACTGGAAGAG 1763
Db      |||||||
QY      361  CGCTTCCAGGGTGAATGGAACTTGAGCCCTGCGCCAAAGGTCATCTCCACACTGGAAGAG 420
Db      |||||||
QY      1764 CCCACCCACAGTGCCTCCACAGCGGCGGAGCCCTGCTGCCGCCACCGCTGTGTCAGC 480
Db      |||||||
QY      421  CCCACCCACAGTGCCTCCACAGCGGCGGAGCCCTGCTGCCGCCACCGCTGTGTCAGC 1823
Db      |||||||
QY      1824 ATTGGTGGGGCAAGGCTGAGGGGGACCTACTCTCCCCCTCTCCATGCTGTCTCCCTG 1883
Db      |||||||
QY      481  ATTGGTGGGGCAAGGCTGAGGGGGACCTACTCTCCCCCTCTCCATGCTGTCTCCCTG 540
Db      |||||||
QY      1884 TGGGCTCACACCGGCACTGTGCATCTACTCTGAGAGATCCCATGGAACACGCCCTGCA 1943
Db      |||||||
QY      541  TGGGCTCACACCGGCACTGTGCATCTACTCTGAGAGATCCCATGGAACACGCCCTGCA 600
Db      |||||||
QY      1944 CGCC 1947
Db      ||||
QY      601 TGCC 604

RESULT 39
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LOCUS      601901840F1 NIH_MGC_19 Homo sapiens mRNA linear EST 21-NOV-2000
DEFINITION mRNA sequence.
ACCESSION BE316292
VERSION   BE316292.1 GI:11264633
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL   National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT   Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1028 row: o column: 09

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High quality sequence stop: 616.
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/clone="IMAGE:4131296"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 178 a 299 c 260 g 161 t
ORIGIN

Query Match 21.9%; Score 597.6; DB 10; Length 898;
Best Local Similarity 95.1%; Pred. No. 4.7e-119;
Matches 715; Conservative 0; Mismatches 24; Indels 13; Gaps 9;

Qy 1655 GTACAGCTTCGGCGCCATCTCCATGCACTGCAACAAAGTCCTCAGCGGTCGCTTCCAGGG 1714
Db 2 GTACAGCTTCGGCGCCATCTCCATGCACTGCAACAAAGTCCTCAGCGGTCGCTTCCAGGG 61

Qy 1715 TGAATGGAACTGCAGCCCTGCCCAAGGTATCTCCACATGGAAGAGCCACCCACCA 1774
Db 62 TGAATGGAACTGCAGCCCTGCCCAAGGTATCTCCACATGGAAGAGCCACCCACCA 121

Qy 1775 GTGCCCCACAGCAGGCGCGAAGCCCTGCTGGCCCCACCGTTGTCAGCATTTGTGGGG 1834
Db 122 GTGCCCCACAGCAGGCGCGAAGCCCTGCTGGCCCCACCGTTGTCAGCATTTGTGGGG 181

Qy 1835 CAAAGGCTGAGGGGGGACCTACTCTCTCCCTCTCCATGCTGTCCCTGTGGGCTCACAC 1894
Db 182 CAAAGGCTGAGGGGGGACCTACTCTCTCCCTCTCCATGCTGTCCCTGTGGGCTCACAC 241

Qy 1895 CGGCACCTGTGACCTACTCTGCGACGATCCCATGGAAGAGCCCTGACGCCCCAGAGTG 1954
Db 242 CGGCACCTGTGACCTACTCTGCGACGATCCCATGGAAGAGCCCTGACGCCCCAGAGTG 301

Qy 1955 AAGGGGCGAGACACGCGCCCTGCTGAGACACCGTCCCAATCCAGCCCTTCTTCCCCCAGG 2014
Db 302 AAGGGGCGAGACACGCGCCCTGCTGAGACACCGTCCCAATCCAGCCCTTCTTCCCCCAGG 360

Qy 2015 GTCCCTGTCATGCTGAGAGGCTGTGGGTGCTGCTGTTGACCTACCTGGACCGAGTGGAC 2074
Db 361 GTCCCTGTCATGCTGAGAGGCTGTGGGTGCTGCTGTTGA-CTACCTGGACCGAGTGGAC 419

Qy 2075 CACAGCTCTGCTCAATTAACCCGGCTGACTCAGTGCGGAGACCGCGACAGTGTGTC 2134
Db 420 CACAGCTCTGCTCAATTAACCCGGCTGACTCAGTGCGGAGACAGCTGACAGTGTGTC 479

Qy 2135 AGGCTCAGCCCTCCGCCAGCCCTGTTCCGCTCACTGGGTGCGCTTCTGGGCTCTGGGAC 2194
Db 480 A-GGTTCAGCCCTCCGCCAGCC--TGTTCCGCTCACTGGGTGTGG-CTGGCTTCTGGGAC 535

Qy 2195 AGGACCATGCTGGGCGGGGTGTGGAATCACCGGGAACCGCCCGCCCGCCCGCCCGCTG 2254
Db 536 AGGACCATGCTGGGCGGGGTGTGGAATCACCGGGAACCGCCCGCCCGCCCG-CCCGCTG 594

Qy 2255 CTCCGGTGTGACAGGGGTGGGGTGGCGCTTAACATTTCCCT-GCTGAGTGTGCTGTG 2313
Db 595 CTCCGGTGTGACAGGGGTGGGGTGGCGCTTAACATTTCCCTGCTGAGTGTGCTGTG 654

Qy 2314 TTTCACAGTGGCGGCTTCCCTGCGAGCGGAGGACGAGCATTTAGCTAGTTAGAGA 2373
Db 655 TGTCAAGTGGCGGGTTCCTGCGACGGAGGGAGGAC--AGGATTTAGCTAGTTAGAGA 712

Qy 2374 CTCGCTGGGAATGTCTCCATTCTCTGAGTAA 2405
Db 713 ATCGCTGGG---AATGGTCCATTCTTGAGTAA 741

RESULT 40
BF311996
LOCUS
DEFINITION BF311996 872 bp mRNA linear EST 21-NOV-2000
601897850F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127172 5',
mRNA sequence.
ACCESSION BF311996
VERSION BF311996.1 GI:11259775
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 872)
NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LUCM1018 row: c column: 13
High quality sequence stop: 684.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 138 a 325 c 240 g 169 t
ORIGIN

Query Match 21.9%; Score 596.8; DB 10; Length 872;
Best Local Similarity 93.7%; Pred. No. 6.9e-119;
Matches 699; Conservative 0; Mismatches 37; Indels 10; Gaps 7;

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Db 2 GTCGCTGTCTCAGCAGTTACCTCTGTTCCTGGAACTCTTCAACCTGCGACGTACTGAA 61

Qy 1649 GGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAAGTCCTCAGCCGTCGCTT 1708
Db 62 GGCCCTGTACAGCTTCGCGCCCATCTCCATGCACTGCAACAAAGTCCTCAGCCGTCGCTT 121

Qy 1709 CCAGGCTGAATGNACTCGAGCCCTGCCCAAGGTATCTCCACATGGAAGAGCCAC 1768
Db 122 CCAGGCTGAATGNACTCGAGCCCTGCCCAAGGTATCTCCACATGGAAGAGCCAC 181

Qy 1769 CCACAGTGGCCCCACAGCGCGCCGAGCCCTGCTGGCCCCACCGTTGTCAGATTGG 1828
Db 182 CCACAGTGGCCCCACAGCGCGCCGAGCCCTGCTGGCCCCACCGTTGTCAGATTGG 241

Qy 1829 TGGGGGCAAGGCTGAGGGGGGACCTACTCTCTCCCTCTCTCCATGCTGTGCTGTGGGC 1888
Db 1829 TGGGGGCAAGGCTGAGGGGGGACCTACTCTCTCCCTCTCTCCATGCTGTGCTGTGGGC 1888

Db 242 TGGGGGAAAGGCTGAGGGGGACCTACTCTCCCTCCTCCATGCTGTCCCTGTGGGC 301
QY 1889 TCACACCGGCACCTGTGCACTCTACTCTGTGGAAGATCCCATGGAACAGCCCTGCACGCCC 1948
Db 302 TCACACCGGCACCTGTGCACTCTACTCTGTGGAAGATCCCATGGAACAGCCCTGCACGCCC 361
QY 1949 AGGATGAAGGGGCGAGACACGCCCCCTGCTGAGACCAAGGTCGAATCCAGCCTTCTTCC 2008
Db 362 AGGATGAAGGGGCGAGACACGCCCCCTGCTGAGACCAAGGTCGAATCCAGCCTTCTTCC 421
QY 2009 CCCAGGTCCTCTGCACTGGCTGAGAGGGGTGNGGGTGCCTGTGTGACCTTACCCCTGGACC-G 2067
Db 422 CCCA-GGTCCCCCTGCATGGCTGAGAGGGGTGTGGGTGCCCTGTGTGACCTTACCCCTGGACCTG 480
QY 2068 AGTGGACACGACCTCGTCCATTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCAC 2127
Db 481 AGTGGACACGACCTCGTCCATTAAACCCGGCTGACTCAGTGCAGGGACAGCCCGCAC 540
QY 2128 GTGGTCCAGGGTCCAGCCCTCCGCGACCCCTGTTCCGCTCACCTGGGTGTGGCTTGGCTT 2187
Db 541 GTGGTCCA-GGTCCAGCCCTCCG-CAGCCCTGTTCCGCTCACCTGGGTGTGGCTTGGCTT 598
QY 2188 CTGGGACAGGCACCATGCTGGGC--CGGGGTGTGGAATCACCGGGAACGCCCCCGCCCC 2245
Db 599 CTGGGACAGGCACCATGCTGGGCCTGGGGTGTGGACTCCCCGGGGAACGCCCCCGCCCC 658
QY 2246 GCGCCGCTGC-TCCGGGTGTGACGGGTGCGGGTGC---GCTTAAACATTTCCCTGCT 2301
Db 659 GCGCTGTGCTTCCGGGTGTGACGGGCGTCCGGGTGCCTTAAACATTTTCCCTGCT 718
QY 2302 GAGTGGCTCGTGTTCACAGTGGGCG 2327
Db 719 GAGTGGCTCCGTGTCCCCAGTGGGCG 744

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Job time : 5099 secs

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